

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 06:58:59 : Search time 27 Seconds
(without alignments)
788.447 Million cell updates/sec

Title: US-10-767-374-2

Perfect score: 321

Sequence: 1 MGLLGLLGLLGLTVDTYGR.....AYIMLCRKTSQEHVYEAAR 321

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 6631800 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	321	100.0	321	4	US-09-254-465A-2
2	137	42.7	306	4	US-09-369-247-63
3	8	2.5	218	4	US-09-252-991A-19931
4	8	2.5	312	2	US-09-014-969-17
5	8	2.5	667	4	US-09-538-082-1307
6	8	2.5	710	4	US-09-252-991A-25375
7	8	2.5	855	2	US-08-938-365-3
8	8	2.5	867	2	US-08-938-365-2
9	8	2.5	954	2	US-08-749-169A-3
10	8	2.5	954	2	US-09-130-032A-3
11	8	2.5	954	4	US-09-866-028-7
12	8	2.5	954	4	US-09-944-457-7
13	8	2.5	955	4	US-09-798-051-8
14	8	2.2	20	2	US-08-078-311-9
15	7	2.2	20	2	US-08-460-402-9
16	7	2.2	24	3	US-08-957-001B-22
17	7	2.2	24	3	US-09-496-301-22
18	7	2.2	49	3	US-09-208-140-5
19	7	2.2	49	3	US-09-208-140-6
20	7	2.2	77	4	US-09-270-767-57911
21	7	2.2	100	4	US-09-134-000C-5929
22	7	2.2	110	4	US-09-248-796A-26879
23	7	2.2	116	1	US-08-053-131-185
24	7	2.2	116	2	US-08-096-762-185
25	7	2.2	117	3	US-09-042-353-48
26	7	2.2	117	3	US-08-758-417A-313
27	7	2.2	125	4	US-09-647-468-159

28	7	2.2	125	4	US-09-647-468-160	Sequence 160, App
29	7	2.2	128	1	US-08-259-372A-14	Sequence 14, Appl
30	7	2.2	128	1	US-08-468-671-14	Sequence 14, Appl
31	7	2.2	128	2	US-08-470-139-8	Sequence 8, Appl
32	7	2.2	128	3	US-09-347-061-8	Sequence 8, Appl
33	7	2.2	128	4	US-09-537-911A-68	Sequence 68, Appl
34	7	2.2	128	4	US-09-855-271-8	Sequence 8, Appl
35	7	2.2	129	1	US-08-217-918-2	Sequence 2, Appl
36	7	2.2	135	4	US-09-582-337-20	Sequence 20, Appl
37	7	2.2	137	4	US-09-582-337-24	Sequence 24, Appl
38	7	2.2	137	4	US-09-270-767-32237	Sequence 32237, A
39	7	2.2	136	4	US-09-328-352-6509	Sequence 6509, Ap
40	7	2.2	170	4	US-09-583-110-2699	Sequence 2699, Ap
41	7	2.2	174	4	US-09-245-764-8	Sequence 8, Appl
42	7	2.2	184	2	US-08-078-311-4	Sequence 4, Appl
43	7	2.2	184	2	US-08-460-402-4	Sequence 4, Appl
44	7	2.2	203	2	US-08-667-939A-20	Sequence 20, Appl
45	7	2.2	203	4	US-08-433-123-20	Sequence 20, Appl
46	7	2.2	215	2	US-08-667-939A-18	Sequence 18, Appl
47	7	2.2	215	4	US-08-433-123-18	Sequence 18, Appl
48	7	2.2	233	2	US-08-667-939A-5	Sequence 5, Appl
49	7	2.2	233	2	US-08-667-939A-6	Sequence 6, Appl
50	7	2.2	233	2	US-08-667-939A-7	Sequence 7, Appl
51	7	2.2	233	2	US-08-667-939A-8	Sequence 8, Appl
52	7	2.2	233	4	US-08-433-123-6	Sequence 6, Appl
53	7	2.2	233	4	US-08-433-123-7	Sequence 7, Appl
54	7	2.2	233	4	US-08-433-123-8	Sequence 8, Appl
55	7	2.2	234	2	US-07-690-192-2	Sequence 2, Appl
56	7	2.2	234	2	US-08-487-550-2	Sequence 2, Appl
57	7	2.2	234	4	US-09-526-098-2	Sequence 2, Appl
58	7	2.2	234	4	US-09-740-002-24	Sequence 24, Appl
59	7	2.2	234	4	US-09-800-029-26	Sequence 26, Appl
60	7	2.2	234	4	US-09-800-729-150	Sequence 150, App
61	7	2.2	234	4	US-09-383-916-2	Sequence 2, Appl
62	7	2.2	235	3	US-08-812-586-16	Sequence 16, Appl
63	7	2.2	235	4	US-09-535-832A-17	Sequence 17, Appl
64	7	2.2	235	4	US-09-800-729-152	Sequence 152, App
65	7	2.2	235	4	US-08-157-101A-5	Sequence 5, Appl
66	7	2.2	236	1	US-08-487-550-10	Sequence 10, Appl
67	7	2.2	236	3	US-09-526-098-10	Sequence 10, Appl
68	7	2.2	236	4	US-09-383-916-10	Sequence 10, Appl
69	7	2.2	239	3	US-08-487-550-6	Sequence 6, Appl
70	7	2.2	239	4	US-09-526-098-6	Sequence 6, Appl
71	7	2.2	239	4	US-09-383-916-6	Sequence 6, Appl
72	7	2.2	240	4	US-09-252-991A-17600	Sequence 17600, A
73	7	2.2	241	2	US-07-916-098A-56	Sequence 56, Appl
74	7	2.2	241	4	US-08-667-939A-2	Sequence 2, Appl
75	7	2.2	254	2	US-08-667-939A-3	Sequence 3, Appl
76	7	2.2	254	2	US-08-667-939A-4	Sequence 4, Appl
77	7	2.2	254	2	US-08-667-939A-9	Sequence 9, Appl
78	7	2.2	254	2	US-08-667-939A-3	Sequence 3, Appl
79	7	2.2	254	4	US-08-433-123-2	Sequence 2, Appl
80	7	2.2	254	4	US-08-433-123-3	Sequence 3, Appl
81	7	2.2	254	4	US-08-433-123-4	Sequence 4, Appl
82	7	2.2	254	4	US-08-433-123-9	Sequence 9, Appl
83	7	2.2	255	4	US-09-107-532A-5758	Sequence 5758, Ap
84	7	2.2	256	4	US-08-078-311-14	Sequence 14, Appl
85	7	2.2	284	2	US-08-078-311-24	Sequence 24, Appl
86	7	2.2	284	2	US-08-460-402-14	Sequence 14, Appl
87	7	2.2	284	2	US-08-460-402-24	Sequence 24, Appl
88	7	2.2	284	2	US-08-460-402-24	Sequence 24, Appl
89	7	2.2	288	4	US-09-134-000C-6445	Sequence 6445, Ap
90	7	2.2	290	4	US-09-540-236-2615	Sequence 2615, Ap
91	7	2.2	291	4	US-09-107-532A-5063	Sequence 5063, Ap
92	7	2.2	307	3	US-08-812-586-2	Sequence 2, Appl
93	7	2.2	307	4	US-09-535-832A-2	Sequence 2, Appl
94	7	2.2	345	4	US-09-457-066-43	Sequence 43, Appl
95	7	2.2	345	4	US-09-564-595D-35	Sequence 35, Appl
96	7	2.2	345	4	US-09-706-868-43	Sequence 43, Appl
97	7	2.2	345	4	US-09-823-033-4	Sequence 4, Appl
98	7	2.2	354	4	US-09-270-767-42600	Sequence 42600, A
99	7	2.2	356	4	US-09-107-532A-4245	Sequence 4245, Ap
100	7	2.2	372	1	US-07-865-878A-4	Sequence 4, Appl

RESULT 4
US-09-014-969-17
; Sequence 17, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,969
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-014-969-17

Query Match 2.5%; Score 8; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILGLILL 10
DB 231 ILGLILL 238

RESULT 5
US-09-538-092-1307
; Sequence 1307, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSegFormatter Version 0.9
; SEQ ID NO 1307
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q13438
US-09-538-092-1307

Query Match 2.5%; Score 8; DB 4; Length 667;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ILGLILLG 11
DB 10 ILGLILLG 17

RESULT 6
US-09-252-991A-25375
; Sequence 25375, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25375
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25375

Query Match 2.5%; Score 8; DB 4; Length 710;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ILGLILLG 11
DB 534 ILGLILLG 541

RESULT 7
US-08-938-365-3
; Sequence 3, Application US/08938365
; Patent No. 5989909
; GENERAL INFORMATION:
; APPLICANT: Yang, Pan
; TITLE OF INVENTION: HUCHORDIN AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,365

FILING DATE: 26-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/040001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 855 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-938-365-3

Query Match 2.5%; Score 8; DB 2; Length 855;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILIG 11
DB 8 LIGLILIG 15

RESULT 8
US-08-938-365-2
Sequence 2, Application US/08938365
Patent No. 5989909

GENERAL INFORMATION:
APPLICANT: Yang, Pan
TITLE OF INVENTION: HUCHORDIN AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,365
FILING DATE: 26-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/040001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-938-365-2

Query Match 2.5%; Score 8; DB 2; Length 867;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILIG 11
DB 13 LIGLILIG 20

RESULT 9
US-08-749-169A-3
Sequence 3, Application US/08749169A
Patent No. 5846770

GENERAL INFORMATION:
APPLICANT: RACIE, Lisa
APPLICANT: LAVALLIE, Edward
APPLICANT: DEROBERTIS, Edward
TITLE OF INVENTION: CHORDIN COMPOSITIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,169A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5284
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-169A-3

Query Match 2.5%; Score 8; DB 2; Length 954;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILIG 11
DB 13 LIGLILIG 20

RESULT 10
US-09-130-032A-3
Sequence 3, Application US/09130032A
Patent No. 5986056

GENERAL INFORMATION:
APPLICANT: Lavallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Derobertis, Edward
TITLE OF INVENTION: HUMAN CHORDIN COMPOSITIONS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive

CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,032A
FILING DATE: August 4, 1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5284-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-130-032A-3

Query Match 2.5%; Score 8; DB 2; Length 954;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 LGALLG 11
Db 13 LGALLG 20

RESULT 11
US-09-866-028-7
Sequence 7, Application US/09866028
Patent No. 6642360
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/866,028
FILING DATE: 2001-05-25
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 7
LENGTH: 954
TYPE: PRT
ORGANISM: Homo Sapien
US-09-866-028-7

Query Match 2.5%; Score 8; DB 4; Length 954;
Best Local Similarity 100.0%; Pred. No. 38;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 4 LGALLG 11
Db 13 LGALLG 20

RESULT 12
US-09-944-457-7
Sequence 7, Application US/09944457
Patent No. 6734288
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,457
FILING DATE: 2001-09-26
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 7
LENGTH: 954
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-457-7

PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. 673428868 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. 673428868 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 7
LENGTH: 954
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-457-7

Query Match 2.5%; Score 8; DB 4; Length 954;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLLG 11
DB 13 LGGLLLG 20

RESULT 13
US-09-798-051-8
Sequence 8, Application US/09798051
Patent No. 6632780
GENERAL INFORMATION:
APPLICANT: Zhang, Ke
APPLICANT: Cam, Linh
APPLICANT: Nakayama, Naoki
TITLE OF INVENTION: Chordin-like-2 Molecules and Uses Thereof
FILE REFERENCE: 01-005
CURRENT APPLICATION NUMBER: US/09/798,051
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 955
TYPE: PRT
ORGANISM: Homo sapiens
US-09-798-051-8

Query Match 2.5%; Score 8; DB 4; Length 955;

Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLLG 11
DB 13 LGGLLLG 20

RESULT 14
US-08-078-311-9
Sequence 9, Application US/08078311
Patent No. 5925750
GENERAL INFORMATION:
APPLICANT: Charon, Martine
APPLICANT: Gieselbrecht, Sylvie
APPLICANT: Penciolelli, Jean-Francois
APPLICANT: Souyri, Michele
APPLICANT: Tambourlin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5925750west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 19-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kowalczyk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.84USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-078-311-9

Query Match 2.2%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
DB 14 LGGLLL 20

RESULT 15
US-08-460-402-9
Sequence 9, Application US/08460402
Patent No. 5989833
GENERAL INFORMATION:

APPLICANT: Charon, Martine
APPLICANT: Gieselbrecht, Silvie
APPLICANT: Penciolelli, Jean-Francois
APPLICANT: Souyri, Michele
APPLICANT: Tambourin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 598933west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,402
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,259
FILING DATE: 20-SEP-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 14-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Randall A. Hillson
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.84US03
TELEPHONE: 612-332-5300
TELECOMMUNICATION INFORMATION:
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-402-9

Query Match 2.2%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
Db 14 LIGLILL 20

RESULT 16
US-08-957-001B-22
Sequence 22, Application US/08957001B
Patent No. 6228621
GENERAL INFORMATION:
APPLICANT: Williams, William V.
APPLICANT: Madalo, Michael
APPLICANT: Weiner, David B.
TITLE OF INVENTION: IMPROVED VACCINES
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: windows
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,001B
FILING DATE: 23-OCT-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,592
FILING DATE: 23-OCT-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-3303
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-957-001B-22

Query Match 2.2%; Score 7; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
Db 9 LIGLILL 15

RESULT 17
US-09-496-301-22
Sequence 22, Application US/09496301
Patent No. 6248565
GENERAL INFORMATION:
APPLICANT: Williams, William V.
APPLICANT: Madalo, Michael
APPLICANT: Weiner, David B.
TITLE OF INVENTION: IMPROVED VACCINES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: windows
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/496,301
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/957,001
FILING DATE: 23-OCT-1997

```
/ APPLICATION NUMBER: US 60/029,592
/ FILING DATE: 23-OCT-1996
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Deluca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: UPN-3303
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-568-3100
/ TELEFAX: 215-568-3439
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 24 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-09-496-301-22

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
   |||||
Db 9 LGGLLL 15

RESULT 18
US-09-208-140-5
/ Sequence 5, Application US/09208140
/ Patent No. 6228576
/ GENERAL INFORMATION:
/ APPLICANT: Del Vecchio, Alfred
/ TITLE OF INVENTION: HEPATITIS C VIRUS NS5B TRUNCATED PROTEIN
/ TITLE OF INVENTION: AND METHODS THEREOF TO IDENTIFY ANTI-VIRAL COMPOUNDS
/ FILE REFERENCE: P50743
/ CURRENT APPLICATION NUMBER: US/09/208,140
/ CURRENT FILING DATE: 1998-12-09
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 5
/ LENGTH: 49
/ TYPE: PRT
/ ORGANISM: Viral
US-09-208-140-5

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
   |||||
Db 31 LGGLLL 37

RESULT 19
US-09-208-140-6
/ Sequence 6, Application US/09208140
/ Patent No. 6228576
/ GENERAL INFORMATION:
/ APPLICANT: Del Vecchio, Alfred
/ TITLE OF INVENTION: HEPATITIS C VIRUS NS5B TRUNCATED PROTEIN
/ TITLE OF INVENTION: AND METHODS THEREOF TO IDENTIFY ANTI-VIRAL COMPOUNDS
/ FILE REFERENCE: P50743
/ CURRENT APPLICATION NUMBER: US/09/208,140
/ CURRENT FILING DATE: 1998-12-09
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 6
/ LENGTH: 49
/ TYPE: PRT
/ ORGANISM: Viral
US-09-208-140-6
```

```
Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
   |||||
Db 31 LGGLLL 37

RESULT 20
US-09-270-767-57911
/ Sequence 57911, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 57911
/ LENGTH: 77
/ TYPE: PRT
/ ORGANISM: Drosophila melanogaster
/ FEATURE:
/ OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57911

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 ATLSTLL 197
   |||||
Db 5 ATLSTLL 11

RESULT 21
US-09-134-000C-5929
/ Sequence 5929, Application US/09134000C
/ Patent No. 6617156
/ GENERAL INFORMATION:
/ APPLICANT: Lynn Doucette-Stamm et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
/ TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 032796-032
/ CURRENT APPLICATION NUMBER: US/09/134,000C
/ CURRENT FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 60/055,778
/ PRIOR FILING DATE: 1997-06-15
/ NUMBER OF SEQ ID NOS: 6812
/ SOFTWARE: Patentln version 3.1
/ SEQ ID NO 5929
/ LENGTH: 100
/ TYPE: PRT
/ ORGANISM: Enterococcus faecalis
US-09-134-000C-5929

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 100;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
   |||||
Db 41 LGGLLL 47

RESULT 22
US-09-248-796A-26879
/ Sequence 26879, Application US/09248796A
/ Patent No. 6747137
```

```

; GENERAL INFORMATION:
; APPLICANT: Kelch Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ. ID NOS: 28208
; SEQ ID NO 26879
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-26879

Query Match      2.2%; Score 7; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      250 PLKATST 256
        |||||
Db      41 PLKATST 47

RESULT 23
; US-08-053-131-185
; Sequence 185, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; MOLECULE TYPE: protein
; US-08-096-762-185
```

```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-053-131-185

Query Match      2.2%; Score 7; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      4 LGLGLLL 10
        |||||
Db      9 LGLGLLL 15

RESULT 24
; US-08-096-762-185
; Sequence 185, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,762
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-096-762-185

Query Match      2.2%; Score 7; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 4 LIGLILL 10
Db 9 LIGLILL 15

RESULT 25
US-09-042-353-48
Sequence 48, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-042-353-48

Query Match 2.2%; Score 7; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
Db 9 LIGLILL 15

RESULT 26
US-08-758-417A-313
Sequence 313, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993

APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 313:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 313:
US-08-758-417A-313

Query Match 2.2%; Score 7; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLLGL 10
DB 9 LGLLGL 15

RESULT 27
US-09-647-468-159
Sequence 159, Application US/09647468
Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHITO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 159
LENGTH: 125
TYPE: PRT
ORGANISM: Mus sp.
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence coding for L chain V region of ant-TF
OTHER INFORMATION: mouse monoclonal antibody ATR-2
US-09-647-468-159

Query Match 2.2%; Score 7; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLLGL 10
DB 5 LGLLGL 11

RESULT 28
US-09-647-468-160
Sequence 160, Application US/09647468
Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH

APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHITO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 160
LENGTH: 125
TYPE: PRT
ORGANISM: Mus sp.
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence coding for L chain V region of ant-TF
OTHER INFORMATION: mouse monoclonal antibody ATR-3
US-09-647-468-160

Query Match 2.2%; Score 7; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLLGL 10
DB 5 LGLLGL 11

RESULT 29
US-08-259-372A-14
Sequence 14, Application US/08259372A
Patent No. 5565354.
GENERAL INFORMATION:
APPLICANT: Osterberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
FILING DATE: 14-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-372A-14

Query Match 2.2%; Score 7; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
DB 7 LGGLLL 13

RESULT 30
US-08-468-671-14
Sequence 14, Application US/08468671
Patent No. 5648077
GENERAL INFORMATION:
APPLICANT: Oseberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.

REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-671-14

Query Match 2.2%; Score 7; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
DB 7 LGGLLL 13

RESULT 31
US-08-470-139-8
Sequence 8, Application US/08470139
Patent No. 5998586
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,139
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TRUJILLO, DOREEN YATKO
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0044
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-470-139-8

Query Match 2.2%; Score 7; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
DB 7 LGGLLL 13

RESULT 32
US-09-347-061-8
Sequence 8, Application US/09347061
Patent No. 6316227
GENERAL INFORMATION:
APPLICANT: Bodmer, Mark
APPLICANT: Ahtwal, Diljeet Singh
APPLICANT: Emtage, John Spencer
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
FILE REFERENCE: CARP-0071
CURRENT APPLICATION NUMBER: US/09/347,061
CURRENT FILING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 128
TYPE: PRT
ORGANISM: Rattus rattus
US-09-347-061-8

Query Match 2.2%; Score 7; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLGLL 10
| | | | |
| | | | |
DB 7 LGLGLL 13

RESULT 33
US-09-537-911A-68
Sequence 68, Application US/09537911A
Patent No. 6451982
GENERAL INFORMATION:
APPLICANT: Chou, Chuan-Chu
APPLICANT: Murgolo, Nicholas
APPLICANT: Abrams, John
APPLICANT: Jenh, Chung-her
APPLICANT: Petro, Mary
APPLICANT: Silver, Jon
APPLICANT: Tindall, Stephen
APPLICANT: Windsor, William
APPLICANT: Zavodny, Paul
TITLE OF INVENTION: Design, Cloning and Expression of Humanized Monoclonal Antibodies
TITLE OF INVENTION: Human Interleukin-5
FILE REFERENCE: JB0233KQ
CURRENT APPLICATION NUMBER: US/09/537,911A
CURRENT FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: 07/832,842
PRIOR FILING DATE: 1992-02-06
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: This antibody contains mouse and human sequences
US-09-537-911A-68

Query Match 2.2%; Score 7; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLGLL 10
| | | | |
| | | | |
DB 7 LGLGLL 13

RESULT 34
US-09-855-271-8
Sequence 8, Application US/09855271
Patent No. 6734286
GENERAL INFORMATION:
APPLICANT: Bodmer, Mark W
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Emtage, John Spencer
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
FILE REFERENCE: CARP-0088
CURRENT APPLICATION NUMBER: US/09/855,271
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/347,061
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1

SEQ ID NO 8
LENGTH: 128
TYPE: PRT
ORGANISM: Rattus rattus
US-09-855-271-8

Query Match 2.2%; Score 7; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLGLL 10
| | | | |
| | | | |
DB 7 LGLGLL 13

RESULT 35
US-08-217-918-2
Sequence 2, Application US/08217918
Patent No. 5506132
GENERAL INFORMATION:
APPLICANT: LAKE, PHILIP
APPLICANT: OSTBERG, LARS
TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,918
FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-217-918-2

Query Match 2.2%; Score 7; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLGLL 10
| | | | |
| | | | |
DB 9 LGLGLL 15

RESULT 36
US-09-582-337-20
Sequence 20, Application US/09582337
Patent No. 6562618
GENERAL INFORMATION:
APPLICANT: Japan Tobacco, Inc.
TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
TITLE OF INVENTION: and Medicinal Uses Thereof
FILE REFERENCE: JI-009PCT

```
/ CURRENT APPLICATION NUMBER: US/09/582,337
/ CURRENT FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: JP P1997-367699
/ PRIOR FILING DATE: 1997-12-25
/ PRIOR APPLICATION NUMBER: JP P1998-356183
/ PRIOR FILING DATE: 1998-12-15
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 20
/ LENGTH: 135
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-582-337-20
```

```
Query Match          2.2%; Score 7; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4  LAGLLLL 10
         |||||
Db       9  LAGLLLL 15
```

```
RESULT 37
US-09-582-337-24
/ Sequence 24, Application US/09582337
/ Patent No. 6562618
/ GENERAL INFORMATION:
/ APPLICANT: Japan Tobacco, Inc.
/ TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
/ FILE REFERENCE: J1-009PCT
/ CURRENT APPLICATION NUMBER: US/09/582,337
/ CURRENT FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: JP P1997-367699
/ PRIOR FILING DATE: 1997-12-25
/ PRIOR APPLICATION NUMBER: JP P1998-356183
/ PRIOR FILING DATE: 1998-12-15
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 24
/ LENGTH: 137
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-582-337-24
```

```
Query Match          2.2%; Score 7; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4  LAGLLLL 10
         |||||
Db       9  LAGLLLL 15
```

```
RESULT 38
US-09-270-767-32237
/ Sequence 32237, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 32237
/ LENGTH: 146
/ TYPE: PRT
/ ORGANISM: Drosophila melanogaster
US-09-270-767-32237
```

```
Query Match          2.2%; Score 7; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      190 VATLSTL 196
         |||||
Db      105 VATLSTL 111
```

```
RESULT 39
US-09-328-352-6509
/ Sequence 6509, Application US/09328352
/ Patent No. 6562958
/ GENERAL INFORMATION:
/ APPLICANT: Gary L. Breton et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
/ FILE REFERENCE: GTC99-03PA
/ CURRENT APPLICATION NUMBER: US/09/328,352
/ CURRENT FILING DATE: 1999-06-04
/ NUMBER OF SEQ ID NOS: 8252
/ SEQ ID NO 6509
/ LENGTH: 166
/ TYPE: PRT
/ ORGANISM: Acinetobacter baumannii
US-09-328-352-6509
```

```
Query Match          2.2%; Score 7; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      229 VVKDSK 235
         |||||
Db      152 VVKDSK 158
```

```
RESULT 40
US-09-583-110-2699
/ Sequence 2699, Application US/09583110
/ Patent No. 6699703
/ GENERAL INFORMATION:
/ APPLICANT: Lynn Doucette-Stamm et al.
/ TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
/ FILE REFERENCE: PAT00-07A
/ CURRENT APPLICATION NUMBER: US/09/583,110
/ CURRENT FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/107,433
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: US 60/085,131
/ PRIOR FILING DATE: 1998-05-12
/ PRIOR APPLICATION NUMBER: US 60/051,553
/ PRIOR FILING DATE: 1997-07-02
/ NUMBER OF SEQ ID NOS: 5322
/ SEQ ID NO 2699
/ LENGTH: 170
/ TYPE: PRT
/ ORGANISM: Streptococcus pneumoniae
US-09-583-110-2699
```

```
Query Match          2.2%; Score 7; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      121 DGNQYR 127
         |||||
Db       87 DGNQYR 93
```

```
RESULT 41
US-09-245-764-8
/ Sequence 8, Application US/09245764
/ Patent No. 6675105
```

GENERAL INFORMATION:
APPLICANT: Hogarth, P. Mark
APPLICANT: Powell, Maree S.
APPLICANT: McKenzie, Ian P.C.
APPLICANT: Maxwell, Kelly F.
APPLICANT: Garrett, Thomas P.J.
APPLICANT: Epa, Vidana
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 4102-4
CURRENT APPLICATION NUMBER: US/09/245,764
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/099,994
EARLIER FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: 60/073,972
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 174
TYPE: PRT
ORGANISM: Homo sapiens
US-09-245-764-8

Query Match 2.2%; Score 7; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 205 DSGSYFC 211
Db 148 DSGSYFC 154

RESULT 42
US-08-078-311-4
Sequence 4, Application US/08078311
Patent No. 5925750
GENERAL INFORMATION:
APPLICANT: Charon, Martine
APPLICANT: Gieselbrecht, Silvie
APPLICANT: Penciolelli, Jean-Francis
APPLICANT: Souyri, Michele
APPLICANT: Tambourin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5925750west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 19-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.84USWO

TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-078-311-4

Query Match 2.2%; Score 7; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
Db 59 LIGLILL 65

RESULT 43
US-08-460-402-4
Sequence 4, Application US/08460402
Patent No. 5989833
GENERAL INFORMATION:
APPLICANT: Charon, Martine
APPLICANT: Gieselbrecht, Silvie
APPLICANT: Penciolelli, Jean-Francis
APPLICANT: Souyri, Michele
APPLICANT: Tambourin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5989833west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,402
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,259
FILING DATE: 20-SEP-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 14-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Randall A. Hillson
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.84US03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-402-4

Query Match 2.2%; Score 7; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLLL 10
Db 59 LGLLL 65

RESULT 44
US-08-667-939A-20
Sequence 20, Application US/08667939A
Patent No. 5998166
GENERAL INFORMATION:
APPLICANT: LUD, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUD-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-667-939A-20

Query Match

Best Local Similarity 2.2%; Score 7; DB 2; Length 203;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 166 DSGSYFC 172

RESULT 45
US-08-433-123-20
Sequence 20, Application US/08433123
Patent No. 6444789
GENERAL INFORMATION:
APPLICANT: LUD, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUD-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-433-123-20

Query Match 2.2%; Score 7; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 166 DSGSYFC 172

RESULT 46
US-08-667-939A-18
Sequence 18, Application US/08667939A
Patent No. 5998166
GENERAL INFORMATION:
APPLICANT: LUD, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUD-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-667-939A-18

Query Match 2.2%; Score 7; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 149 DSGSYFC 155

RESULT 47
US-08-433-123-18:

; Sequence 18, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LEO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LEO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-433-123-18

Query Match 2.2%; Score 7; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 149 DSGSYFC 155

RESULT 48
US-08-667-939A-5
; Sequence 5, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LEO, Shun

; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LEO=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-667-939A-5

Query Match 2.2%; Score 7; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 166 DSGSYFC 172

RESULT 49
US-08-667-939A-6
; Sequence 6, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LEO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUD-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-667-939A-6

Query Match 2.2%; Score 7; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
|||
Db 166 DSGSYFC 172

RESULT 50
US-08-667-939A-7
Sequence 7, Application US/08667939A
Patent No. 5998166
GENERAL INFORMATION:
APPLICANT: LUD, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUD-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-667-939A-7

Query Match 2.2%; Score 7; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
|||
Db 166 DSGSYFC 172

RESULT 51
US-08-667-939A-8
Sequence 8, Application US/08667939A
Patent No. 5998166
GENERAL INFORMATION:
APPLICANT: LUD, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUD-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-667-939A-8

Query Match 2.2%; Score 7; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
|||
Db 166 DSGSYFC 172

RESULT 52
US-08-433-123-5
Sequence 5, Application US/08433123
Patent No. 6444789
GENERAL INFORMATION:
APPLICANT: LUD, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/433,123
FILING DATE: 514
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LWO=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-5

Query Match 2.2%; Score 7; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
DB 166 DSGSYFC 172

RESULT 53
US-08-433-123-6
Sequence 6, Application US/08433123
Patent No. 6444789
GENERAL INFORMATION:
APPLICANT: LWO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LWO=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-6

Query Match 2.2%; Score 7; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
DB 166 DSGSYFC 172

RESULT 54
US-08-433-123-7
Sequence 7, Application US/08433123
Patent No. 6444789
GENERAL INFORMATION:
APPLICANT: LWO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LWO=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-7

Query Match 2.2%; Score 7; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
DB 166 DSGSYFC 172

RESULT 55
US-08-433-123-8
Sequence 8, Application US/08433123
Patent No. 6444789
GENERAL INFORMATION:
APPLICANT: LWO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-8

Query Match 2.2%; Score 7; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 166 DSGSYFC 172

RESULT 56
US-07-690-192-2
Sequence 2, Application US/07690192
Patent No. 5919650
GENERAL INFORMATION:
APPLICANT: Montano, Ximena
TITLE OF INVENTION: METHOD FOR INACTIVATION OF PROTEIN
TITLE OF INVENTION: FUNCTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/690,192
FILING DATE: 19910422
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bogden, James M.
REGISTRATION NUMBER: 32,962
REFERENCE/DOCKET NUMBER: DC13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 921-4163
TELEFAX: (609) 921-4526
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-690-192-2

Query Match 2.2%; Score 7; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
Db 7 LIGLILL 13

RESULT 57
US-08-487-550-2
Sequence 2, Application US/08487550
Patent No. 613898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-2

Query Match 2.2%; Score 7; DB 3; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
Db 7 LIGLILL 13

RESULT 58
US-09-526-098-2
Sequence 2, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
US-09-526-098-2


```

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teeklin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-526-098-2

Query Match      2.2%; Score 7; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LGLGLLL 10
        |||||
Db       7 LGLGLLL 13

RESULT 59
US-09-740-002-24
; Sequence 24, Application US/09740002
; Patent No. 6537809
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-24

Query Match      2.2%; Score 7; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      4 LGLGLLL 10
        |||||
Db       7 LGLGLLL 13

RESULT 60
US-09-740-002-26
; Sequence 26, Application US/09740002
; Patent No. 6537809
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-26

Query Match      2.2%; Score 7; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LGLGLLL 10
        |||||
Db       9 LGLGLLL 15

RESULT 61
US-09-800-729-150
; Sequence 150, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: N1 et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 150
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (120)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-800-729-150

Query Match      2.2%; Score 7; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 62
US-09-383-916-2
Sequence 2, Application US/09383916
Patent No. 6709654
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,916
FILING DATE: 26-AUG-1999
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teakin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-383-916-2

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
|||||
Db 7 LGGLLL 13

RESULT 63
US-08-812-586-16
Sequence 16, Application US/08812586
Patent No. 6048704
GENERAL INFORMATION:
APPLICANT: Martin David, Tilson
TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSER: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,586
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/53862-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-812-586-16

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
|||||
Db 9 LGGLLL 15

RESULT 64
US-09-535-832A-17
Sequence 17, Application US/09535832A
Patent No. 6537769
GENERAL INFORMATION:
APPLICANT: Tilson, Martin David
TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
TITLE OF INVENTION: Diagnostic and Therapeutic Use Thereof
FILE REFERENCE: 53862-AZ
CURRENT APPLICATION NUMBER: US/09/535,832A
CURRENT FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-535-832A-17

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
|||||
Db 9 LGGLLL 15

RESULT 65
US-09-800-729-152
Sequence 152, Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013

PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 152
LENGTH: 235
TYPE: PROT
ORGANISM: Homo sapiens
US-09-800-729-152

Query Match 2.2%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
DB 9 LIGLILL 15

RESULT 66
US-08-157-101A-5
Sequence 5, Application US/08157101A
Patent No. 5808032
GENERAL INFORMATION:
APPLICANT: KURIHARA, TATSUYA
APPLICANT: MATSUKURA, SHIGEKAZU
APPLICANT: TSURUOKA, NOBUO
APPLICANT: ARIWA, KENJI
APPLICANT: NISHIHARA, TATSURO
TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION
TITLE OF INVENTION: PLASMIDS THEREFOR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 35843
REFERENCE/DOCKET NUMBER: 9437/204199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEFAX: 202-822-0944
TELEX: 6714627 CUCH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-157-101A-5

Query Match 2.2%; Score 7; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
DB 9 LIGLILL 15

RESULT 67
US-08-487-550-10
Sequence 10, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teekio, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-10

Query Match 2.2%; Score 7; DB 3; Length 236;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
DB 7 LIGLILL 13

RESULT 68
US-09-526-098-10
Sequence 10, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teeklin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-526-098-10

Query Match 2.2%; Score 7; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
Db 7 LIGLILL 13

RESULT 69
US-09-383-916-10
Sequence 10, Application US/09383916
Patent No. 6709654
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,916
FILING DATE: 26-AUG-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teeklin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-383-916-10

Query Match 2.2%; Score 7; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
Db 7 LIGLILL 13

RESULT 70
US-08-487-550-6
Sequence 6, Application US/08487550
Patent No. 613898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teeklin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-6

US-08-487-550-6

Query Match 2.2%; Score 7; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
Db 7 LIGLILL 13

RESULT 71
US-09-526-098-6
Sequence 6, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONOXY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teeklin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-526-098-6

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 239;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ILGLLL 10
Db 7 ILGLLL 13

RESULT 72
US-09-383-916-6
Sequence 6, Application US/09383916
Patent No. 6709654
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONOXY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,916
FILING DATE: 26-AUG-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teeklin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-383-916-6

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 239;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ILGLLL 10
Db 7 ILGLLL 13

RESULT 73
US-09-252-991A-17600
Sequence 17600, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17600
LENGTH: 240
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17600

Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Length 240;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILGLLL 9
Db 48 ILGLLL 54

RESULT 74
US-07-916-098A-56
Sequence 56, Application US/07916098A
Patent No. 5871732
GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.

;; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
;; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
;; NUMBER OF SEQUENCES: 61
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
;; STREET: 10 SOUTH WACKER DRIVE
;; CITY: CHICAGO
;; STATE: ILLINOIS
;; COUNTRY: U.S.A.
;; ZIP: 60606
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WORD PERFECT 5.1
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/916,098A
;; FILING DATE: July 24, 1992
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US91/08843
;; FILING DATE: No. 5871732ember 27, 1991
;; CLASSIFICATION: 424
;; APPLICATION NUMBER: 07/618,542
;; FILING DATE: No. 5871732ember 27, 1990
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: JOHN J. MC DONNELL
;; REGISTRATION NUMBER: 26,949
;; REFERENCE/DOCKET NUMBER: 92,310-G
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 715-1000
;; TELEFAX: (312) 715-1234
;; TELEX: 910/221-5317
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 241 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-07-916-098A-56

Query Match 2.2%; Score 7; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||
DB 9 LIGLILL 15

RESULT 75
US-09-489-039A-8330
; Sequence 8330, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8330
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8330

Query Match 2.2%; Score 7; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LIGLILL 10
|||
DB 15 LIGLILL 21

Search completed: January 4, 2005, 07:00:03
Job time : 29 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 06:58:59 ; Search time 115 Seconds

(without alignments)
1606.046 Million cell updates/sec

Title: US-10-767-374-2

Perfect score: 321
Sequence: 1 MGILLGLLGLHGLTVDTYGR.....AYIMLCRKTSQEHVYEAAR 321Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 100 summaries

Database : Uniprot 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	321	100.0	321	2	OGUX14
2	321	100.0	321	2	AAQ88707
3	321	100.0	399	2	Q9Y279
4	16	5.0	280	2	OB0WA3
5	16	5.0	280	2	BAC30780
6	9	2.8	178	2	Q72L88
7	9	2.8	178	2	AA880489
8	8	2.5	124	1	WFD2_CANFA
9	8	2.5	142	2	Q7ME51
10	8	2.5	217	2	Q8PI21
11	8	2.5	222	2	Q8ENJ3
12	8	2.5	223	2	Q91JY1
13	8	2.5	240	1	MTRA_METRA
14	8	2.5	240	1	MTRA_METRA
15	8	2.5	240	1	MTRA_METRA
16	8	2.5	249	2	Q6XPU4
17	8	2.5	249	2	AAAP4530
18	8	2.5	265	2	Q66648
19	8	2.5	265	2	Q95KP8
20	8	2.5	269	2	Q95KP9
21	8	2.5	271	2	Q95KQ0
22	8	2.5	292	2	Q6SFH9
23	8	2.5	292	2	AA838238
24	8	2.5	346	2	Q702H2
25	8	2.5	346	2	CA828454
26	8	2.5	350	2	Q9GJ53
27	8	2.5	366	2	Q6TUV6
28	8	2.5	366	2	AA807413
29	8	2.5	412	2	Q30187
30	8	2.5	520	1	PSL2_HUMAN
31	8	2.5	537	2	Q7QIR0

32	8	2.5	590	2	Q6BSF5	Q6BSF5
33	8	2.5	595	1	SILL_HUMAN	Q96PQ1 homo sapien
34	8	2.5	597	1	SILL_PANTR	Q951H1 pan troglod
35	8	2.5	612	2	Q6IBL2	Q6IBL2 homo sapien
36	8	2.5	612	2	Q9BW99	Q9BW99 homo sapien
37	8	2.5	612	2	CAG33072	CAG33072 homo sapien
38	8	2.5	655	2	Q6JH13	Q6JH13 babesia bov
39	8	2.5	655	2	AA858045	AA858045 babesia b
40	8	2.5	667	1	Q9_HUMAN	Q9_HUMAN
41	8	2.5	750	2	Q72TS9	Q72TS9
42	8	2.5	752	2	AA869549	AA869549 leptospira
43	8	2.5	937	2	Q8FLB6	Q8FLB6 leptospira
44	8	2.5	948	1	CHRD_MOUSE	Q92062 mus musculu
45	8	2.5	954	2	Q6UM63	Q6UM63 homo sapien
46	8	2.5	954	2	AAQ89285	AAQ89285 homo sapi
47	8	2.5	955	1	CHRD_HUMAN	Q9H2X0 homo sapien
48	8	2.5	975	2	Q86G86	Q86G86 pseudoplusi
49	8	2.2	20	1	CPBX_CAVPO	P34033 cavia porce
50	8	2.2	31	2	Q9QVA5	Q9QVA5 cavia (guin
51	8	2.2	33	2	Q9QVA4	Q9QVA4 cavia (guin
52	8	2.2	41	2	Q9QVY1	Q9QVY1 cavia (guin
53	8	2.2	42	2	Q70BW1	Q70BW1 sus scrofa
54	8	2.2	42	2	Q70BW2	Q70BW2 sus scrofa
55	8	2.2	42	2	CAE52545	CAE52545 sus scrof
56	8	2.2	42	2	CAE52547	CAE52547 sus scrof
57	8	2.2	44	2	Q9UN20	Q9UN20 homo sapien
58	8	2.2	66	2	Q8U2N4	Q8U2N4 pyrococcus
59	8	2.2	70	2	Q72H08	Q72H08 thermus t
60	8	2.2	70	2	AA882029	AA882029 thermus t
61	8	2.2	77	2	Q8TEA2	Q8TEA2 homo sapien
62	8	2.2	85	2	Q7UT23	Q7UT23 rhodospirill
63	8	2.2	88	2	Q8FEV3	Q8FEV3 escherichia
64	8	2.2	92	2	Q8KAN9	Q8KAN9 mus musculu
65	8	2.2	95	2	Q83JU5	Q83JU5 enterococcu
66	8	2.2	97	2	Q16755	Q16755 homo sapien
67	8	2.2	97	2	Q8GK66	Q8GK66 arabidopsis
68	8	2.2	98	2	Q950U7	Q950U7 rhizophyali
69	8	2.2	100	2	Q8Q355	Q8Q355 gallus galli
70	8	2.2	101	1	YGVA_YEAST	P53089 saccharomyc
71	8	2.2	101	2	AA856831	AA856831 saccharom
72	8	2.2	105	1	PLF4_RAT	P06765 rattus norv
73	8	2.2	105	2	Q70HT8	Q70HT8 mycoplasma
74	8	2.2	105	2	CAE45730	CAE45730 mycoplasma
75	8	2.2	105	2	CAE45731	CAE45731 mycoplasma
76	8	2.2	117	1	Q8LMS8	Q8LMS8 oryza sativ
77	8	2.2	117	1	KVLI_HUMAN	P01601 homo sapien
78	8	2.2	117	1	KVLI_HUMAN	P01602 homo sapien
79	8	2.2	118	2	Q70HT1	Q70HT1 mycoplasma
80	8	2.2	118	2	Q70HT4	Q70HT4 mycoplasma
81	8	2.2	118	2	CAE45735	CAE45735 mycoplasma
82	8	2.2	118	2	CAE45736	CAE45736 mycoplasma
83	8	2.2	118	2	CAE45738	CAE45738 mycoplasma
84	8	2.2	119	2	Q6USAT	Q6USAT saccharum h
85	8	2.2	119	2	AAQ95639	AAQ95639 saccharum
86	8	2.2	121	2	Q8CR98	Q8CR98 brachylococ
87	8	2.2	121	2	WFD2_RABIT	Q86B31 oryctolagus
88	8	2.2	126	2	Q67392	Q67392 aquilex aeo
89	8	2.2	127	2	Q9AGW6	Q9AGW6 nostoc punc
90	8	2.2	127	2	Q80Z00	Q80Z00 mus musculu
91	8	2.2	127	2	Q9DAK7	Q9DAK7 mus musculu
92	8	2.2	128	2	Q8C355	Q8C355 mus musculu
93	8	2.2	129	1	KVLI_HUMAN	P04433 homo sapien
94	8	2.2	129	1	KVLI_HUMAN	P04433 homo sapien
95	8	2.2	130	2	Q89U61	Q89U61 bradyrhizob
96	8	2.2	133	2	Q84BX3	Q84BX3 mycoplasma
97	8	2.2	138	2	Q73UT4	Q73UT4 mycobacteri
98	8	2.2	138	2	AA805820	AA805820 mycobacte
99	8	2.2	139	2	Q72IU6	Q72IU6 thermus the
100	8	2.2	139	2	Q72IU6	Q72IU6 thermus the

ALIGNMENTS

```
RESULT 1
AO88707 PRELIMINARY; PRT; 321 AA.
ID Q6UX14
AC Q6UX14;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE STIGMA.
GN ORFNames=UNQ317;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887236; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.B., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358341; AAQ8707.1; -.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR003110; IG_1like.
DR InterPro; IPR003598; IG_2.
DR InterPro; IPR003596; IG_2.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG_2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 2.
SQ SEQUENCE 321 AA; 35544 MW; B2AB2E3151D39C6E CRC64;

Query Match 100.0%; Score 321; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLGLHTVDTYGRPILEVESVTGPKGVDNLPCTYDPLQGYQVLYKLVOR 60
DB 1 MGILLGLLGLHTVDTYGRPILEVESVTGPKGVDNLPCTYDPLQGYQVLYKLVOR 60
QY 61 GSDPVITFLRDSGDHIIQAKYQGRHLVSHKVPDVSLSQSTLEMDRSHYTCENTWQTP 120
DB 61 GSDPVITFLRDSGDHIIQAKYQGRHLVSHKVPDVSLSQSTLEMDRSHYTCENTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRISLQCARGSPPISYIWKQ 180
DB 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRISLQCARGSPPISYIWKQ 180
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRISLQCARGSPPISYIWKQ 180
DB 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRISLQCARGSPPISYIWKQ 180
QY 181 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKFPVVKDSKLLKTK 240
DB 181 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKFPVVKDSKLLKTK 240
QY 181 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKFPVVKDSKLLKTK 240
DB 181 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKFPVVKDSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKSQMDWTMDGYLGSTSGAPGKSLPVPFAIIILISLCMVVFT 300
DB 241 TEAPTTMTYPLKATSTVKSQMDWTMDGYLGSTSGAPGKSLPVPFAIIILISLCMVVFT 300
QY 301 MAYIMLCRKTSQGEHYVEAAR 321
DB 301 MAYIMLCRKTSQGEHYVEAAR 321
RESULT 2
AAQ88707
```

```
ID AAQ88707 PRELIMINARY; PRT; 321 AA.
AC AAQ88707;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE STIGMA.
GN UNQ317.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.B., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment."
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358341; AAQ8707.1; -.
SQ SEQUENCE 321 AA; 35544 MW; B2AB2E3151D39C6E CRC64;

Query Match 100.0%; Score 321; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLGLHTVDTYGRPILEVESVTGPKGVDNLPCTYDPLQGYQVLYKLVOR 60
DB 1 MGILLGLLGLHTVDTYGRPILEVESVTGPKGVDNLPCTYDPLQGYQVLYKLVOR 60
QY 61 GSDPVITFLRDSGDHIIQAKYQGRHLVSHKVPDVSLSQSTLEMDRSHYTCENTWQTP 120
DB 61 GSDPVITFLRDSGDHIIQAKYQGRHLVSHKVPDVSLSQSTLEMDRSHYTCENTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRISLQCARGSPPISYIWKQ 180
DB 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRISLQCARGSPPISYIWKQ 180
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRISLQCARGSPPISYIWKQ 180
DB 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRISLQCARGSPPISYIWKQ 180
QY 181 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKFPVVKDSKLLKTK 240
DB 181 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKFPVVKDSKLLKTK 240
QY 181 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKFPVVKDSKLLKTK 240
DB 181 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKFPVVKDSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKSQMDWTMDGYLGSTSGAPGKSLPVPFAIIILISLCMVVFT 300
DB 241 TEAPTTMTYPLKATSTVKSQMDWTMDGYLGSTSGAPGKSLPVPFAIIILISLCMVVFT 300
QY 301 MAYIMLCRKTSQGEHYVEAAR 321
DB 301 MAYIMLCRKTSQGEHYVEAAR 321
RESULT 3
Q9Y279 PRELIMINARY; PRT; 399 AA.
ID Q9Y279;
AC Q9Y279;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Z391g protein precursor (Ig superfamily protein).
GN Name=Z391g; Synonyms=Z391G;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
```


RP SEQUENCE FROM N.A.
 RX MEDLINE=20461865; PubMed=11004523;
 RA Langmead K., Colledge L., Kloos D.U., Fontes M., Wiesacker P.,
 RT "Cloning of 2391g, a novel gene with immunoglobulin-like domains
 located on human chromosome X.";
 RL Biochim. Biophys. Acta 1492:522-525(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strauberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ315502; CAB51536.1; -
 DR EMBL; BC010525; AAH10525.1; -
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 KM Signal.
 FT CHAIN 1 19 Potential.
 FT 20 399 2391g protein.
 SQ SEQUENCE 399 AA; 43987 MW; 735CA3BC58185035 CRC64;
 Query Match 100.0%; Score 321; DB 2; Length 399;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 301 MAYIMLCRKTSGQEHVEAAR 321
 RESULT 4
 ID 080WA3 PRELIMINARY; PRT; 280 AA.
 AC 080WA3;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein BC025105.
 GN Name=BC025105;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RA Strauberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025105; AAH25105.1; -
 DR MGD; MGI:2679720; BC025105.
 DR InterPro; IPR007110; Ig-like.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 280 AA; 31467 MW; 3F099A8996CE8977 CRC64;
 Query Match 5.0%; Score 16; DB 2; Length 280;
 Best Local Similarity 100.0%; Pred. No. 16e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 110 HYTCVWTQTPDGNV 125
 RESULT 5
 ID BAC30780 PRELIMINARY; PRT; 280 AA.
 AC BAC30780;
 DT 14-APR-2004 (TREMBlrel. 27, Created)
 DT 14-APR-2004 (TREMBlrel. 27, Last sequence update)
 DT 14-APR-2004 (TREMBlrel. 27, Last annotation update)
 DE Adult male aorta and vein cDNA, RIKEN full-length enriched library,
 DE clone:A530061A1 product:hypothetical immunoglobulin and major
 DE histocompatibility complex domain/immunoglobulin subtype containing
 DE protein, full insert sequence.
 OS Mus musculus (Mouse).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=22354683; PubMed=1246851;
 RA The PANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P.; Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=2049374; PubMed=11042159;
 RA Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.;
 RA Kono H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K.; Itoh M.; Aizawa K.; Nagata S.; Sasaki N.; Carninci P.;
 RA Kono H.; Akiyama J.; Nishi K.; Kiteuchi T.; Tashiro H.; Itoh M.;
 RA Sumi N.; Ishii Y.; Nakamura S.; Hazama M.; Nishine T.; Harada A.;
 RA Yamamoto R.; Matsumoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.;
 RA Fujiwaki S.; Inoue K.; Togawa Y.; Izawa M.; Ohara E.; Watanishi M.;
 RA Yoneda Y.; Ishikawa T.; Ozawa K.; Tanaka T.; Matsumura S.; Kawai J.;
 RA Okazaki Y.; Muramatsu M.; Inoue Y.; Kira A.; Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA Adachi J.; Aizawa K.; Akimura T.; Arakawa T.; Bono H.; Carninci P.;
 RA Fukuda S.; Furuno M.; Hanagaki T.; Hara A.; Hashizume W.;
 RA Hayashida K.; Hayatsu N.; Hiramoto K.; Hiraoka T.; Hirozane T.;
 RA Hori F.; Imotani K.; Ishii Y.; Itoh M.; Kaga I.; Kasukawa T.;
 RA Katoh H.; Kawai J.; Kojima Y.; Kondo S.; Kono H.; Kouda M.; Koya S.;
 RA Kurihara C.; Matsuyama T.; Miyazaki A.; Murata M.; Nakamura M.;
 RA Nishi K.; Nomura K.; Numazaki R.; Ohno M.; Ohnato N.; Okazaki Y.;
 RA Saito R.; Saitoh H.; Sakai C.; Sakai K.; Sakazume N.; Sano H.;
 RA Sasaki D.; Shibata K.; Shinagawa A.; Shiraki T.; Sogabe Y.; Tagami M.;
 RA Tagawa A.; Takahashi F.; Takeku-Akahira S.; Takeda Y.; Tanaka T.;
 RA Tomaru A.; Toyota T.; Yasunishi A.; Muramatsu M.; Hayashizaki Y.;
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; ARO41014; BAC30780.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 280 AA; 31467 MW; 3F099AE996CE8977 CRC64;
 QY

Db 110 HYTCVWQTPDGNV 125
 |||||
 RESULT 6
 ID Q72LB8 PRELIMINARY; PRT; 178 AA.
 AC Q72LB8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=TTCC0141;
 OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 NCBI_TaxID=262724;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=15064768;
 RA Henne A.; Brueggemann H.; Raasch C.; Wlezer A.; Hartsch T.;
 RA Liesegang H.; Johann A.; Lienard T.; Gohl O.; Martinez-Arias R.;
 RA Jacobi C.; Starkuviene V.; Schlenzcek S.; Dencker S.; Huber R.;
 RA Klenk H.-P.; Kramer W.; Merkl R.; Gottschalk G.; Fritze H.-J.;
 RT "The genome sequence of the extreme thermophile Thermus
 RT thermophilus."
 RL Nat. Biotechnol. 22:547-553(2004).
 DR EMBL; AEO17301; AAS80489.1; -.
 DR InterPro; IPR000252; DedA; 1.
 DR Pfam; PF00597; DedA; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 178 AA; 19199 MW; AD34F4CC5250AB68 CRC64;
 QY
 |||||
 Db 156 ILGLLLG 164
 |||||
 RESULT 7
 ID AAS80489 PRELIMINARY; PRT; 178 AA.
 AC AAS80489;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 11-MAY-2004 (TrEMBLrel. 27, Last sequence update)
 DT 11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN TTC0141.
 OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 NCBI_TaxID=262724;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=15064768;
 RA Henne A.; Brueggemann H.; Raasch C.; Wlezer A.; Hartsch T.;
 RA Liesegang H.; Johann A.; Lienard T.; Gohl O.; Martinez-Arias R.;
 RA Jacobi C.; Starkuviene V.; Schlenzcek S.; Dencker S.; Huber R.;
 RA Klenk H.-P.; Kramer W.; Merkl R.; Gottschalk G.; Fritze H.-J.;
 RT "The genome sequence of the extreme thermophile Thermus
 RT thermophilus."
 RL Nat. Biotechnol. 22:547-553(2004).
 DR EMBL; AEO17301; AAS80489.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 178 AA; 19199 MW; AD34F4CC5250AB68 CRC64;
 QY
 |||||
 Db 156 ILGLLLG 164
 |||||
 Query Match 2.8%; Score 9; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query Match 2.8%; Score 9; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ILGLLLLG 11
 DB 156 ILGLLLLG 164

RESULT 8
 WFD2_CANFA STANDARD; PRT: 124 AA.

AC Q28654; 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE WAP four-disulfide core domain protein 2 precursor (Major epididymis-specific protein E4) (CE4) (Epididymal secretory protein E4).
 GN Name=WFD2;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Epididymis;
 RX MEDLINE=95263175; PubMed=7744511;
 RA Ellendrock K., Pera I., Hartung S., Ivell R.;
 RT "Gene expression in the dog epididymis: a model for human epididymal function";
 RL Int. J. Androl. 17:314-323(1994).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=95263176; PubMed=7744512;
 RA Pera I., Ivell R., Kirchoff C.;
 RT "Regional variation of specific gene expression in the dog epididymis as revealed by in-situ transcript hybridization";
 RL Int. J. Androl. 17:324-330(1994).
 CC -1- FUNCTION: Possible function in sperm maturation.
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- TISSUE SPECIFICITY: Epididymis. Highest levels are found in the caput and proximal cauda regions. Lower levels in the distal cauda. Not detected in the efferent ducts.
 CC -1- SIMILARITY: Contains 2 WAP-type domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL, S77395; AAB34264.1; -.
 DR PIR, I54768; I54768.
 DR HSSP, O46655; ICJH.
 DR InterPro, IPR008198; Prot_inh_antileu.
 DR InterPro, IPR008197; WAP.
 DR Pfam, PF00095; WAP; 2.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR ProDom, PD001224; WAP_C; 1.
 DR SMART, SM00217; WAP; 2.
 DR PROSITE, PS00317; 4_DISULFIDE_CORE; 2.
 DR KMW GlycoProtein, Repeat; Serine protease inhibitor; signal.
 FT SIGNAL 1 27
 FT CHAIN 28 124 WAP four-disulfide core domain protein 2.
 FT DOMAIN 32 74 WAP 1.
 FT DOMAIN 76 124 WAP 2.
 FT DISULFID 36 62 By similarity.
 FT DISULFID 45 66 By similarity.
 FT DISULFID 49 61 By similarity.
 FT DISULFID 55 70 By similarity.
 FT DISULFID 80 110 By similarity.
 FT DISULFID 93 114 By similarity.
 FT DISULFID 97 109 By similarity.
 FT DISULFID 103 119 By similarity.
 FT CARBOHYD 44 44 N-linked (GlcNAc...) (Potential).

SO SEQUENCE 124 AA; 12951 MW; 15AFA315BA13958C CRC64;

Query Match
 Best Local Similarity 2.5%; Score 8; DB 1; Length 124;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ILGLLLLG 11
 DB 14 ILGLLLLG 21

RESULT 9

ID Q7ME51 PRELIMINARY; PRT: 142 AA.

AC Q7ME51; 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hypothetical protein VVA0834.
 GN Name=VVA0834;
 OS Vibrio vulnificus (strain VJ016).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=196600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14636965;
 RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C., Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L., Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
 RT "Comparative genome analysis of *Vibrio vulnificus*, a marine pathogen";
 RL Genome Res. 13:2577-2587(2003).
 DR EMBL, AP005347; BAC96859.1; -.
 KW Hypothetical protein.

SO SEQUENCE 142 AA; 16151 MW; 7A69E81D772310F5 CRC64;

Query Match
 Best Local Similarity 2.5%; Score 8; DB 2; Length 142;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 308 RKTSGQEH 315
 DB 126 RKTSGQEH 133

RESULT 10
 ID Q8PIZ1 PRELIMINARY; PRT: 217 AA.

AC Q8PIZ1; 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Lipoprotein.
 GN OrderedLocustNames=XAC2753;
 OS Xanthomonas axonopodis (pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=92829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Petro J.A., Reinach F.C., Farah C.S., Furlan L.R., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., de Azevedo A.M., Bertolini M.C., Camargo L.E.A., Camarotte G., Camarvan F., Cardoso J., Chambergos J.R., Clapina L.P., Clearelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A., Katsuyama A.M., Kishitani L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Trufi D., Tsal S.M., White F.F.,
 RA Setudal J.C., Kitajima J.P.,
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities";
 RL Nature 417:459-463(2002).
 DR EMBL: A6011915; AAM37599.1; -;
 DR InterPro: IPR000064; NLP_P60.
 DR Pfam: PF00877; NLP_P60; 1.
 KW Complete proteome; Lipoprotein.
 SQ SEQUENCE 217 AA; 22884 MW; 4D053E7BA92819B0 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 217;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ILGLILLG 11
 DB 56 ILGLILLG 63

RESULT 11
 O8ENU3 PRELIMINARY; PRT; 222 AA.
 ID O8ENU3;
 AC O8ENU3;
 DT 01-MAR-2003 (TEMBLrel. 23, Created)
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE ABC transporter permease.
 GN OrderedlocusNames=OB2383;
 OS Oceanobacillus iheyensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
 NC NCBI_TaxID=182710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=HTE831;
 RC MEDLINE=2220767; PubMed=12235376;
 RA Takami H., Takaki Y., Uchiyama I.,
 RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
 RT Ridge and its unexpected adaptive capabilities to extreme
 RT environments";
 RL Nucleic Acids Res. 30:3927-3935(2002).
 CC -1- FUNCTION: Part of a binding-protein-dependent transport system.
 CC -1- Probably responsible for the translocation of the substrate across
 CC the membrane (by similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport
 CC system permease family.
 DR EMBL: AP004601; BAC14339.1; -;
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005215; F:transporter activity; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR000515; BPD_transp.
 DR Pfam: PF00528; BPD_transp.1; 1.
 DR PROSITE: PS50928; ABC_TM1; 1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 222 AA; 24338 MW; A64DBEDBF4B885D CRC64;

Query Match 2.5%; Score 8; DB 2; Length 222;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILGLILL 9
 DB 36 GILGLILL 43

RESULT 12
 O911J1 PRELIMINARY; PRT; 223 AA.
 ID O911J1;
 AC O911J1;

DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedlocusNames=PA2284;
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 NC NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Hickey C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Conlter S.N., Folger K.R., Kae A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen";
 RL Nature 406:959-964(2000).
 DR EMBL: A6004654; AAG05672.1; -;
 DR PIR: H83359; H83359.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 223 AA; 23599 MW; 4EE4632BD82AF0DB CRC64;

Query Match 2.5%; Score 8; DB 2; Length 223;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ILGLILLG 11
 DB 47 ILGLILLG 54

RESULT 13
 ID MTNA METAC
 AC O8TU03;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Tetrahydromethanopterin S-methyltransferase subunit A (EC 2.1.1.86)
 DE (N5-methyltetrahydromethanopterin--coenzyme M methyltransferase
 DE subunit A).
 GN Name=mta; OrderedlocusNames=MA0272;
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 NC NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZA / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/97.223902;
 RA Galleagan J.E., Nusbbaum C., Roy A., Endrizzi M.G., Macdonald P.,
 RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atchop D., Brown A.,
 RA Allen N., Naylor J., Stange-Thomann N., DeArrelino K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D., Brown A.,
 RA Hedderich R., Ingram-Smith C., Kuetner H.C., Kzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Slinger T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
 RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birren B.;
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
 RT and physiological diversity";
 RL Genome Res. 12:532-542(2002).
 CC -1- FUNCTION: Part of a complex that catalyzes the formation of
 CC methyl-coenzyme M and tetrahydromethanopterin from coenzyme M and
 CC methyl-tetrahydromethanopterin. This is an energy-conserving,
 CC sodium-ion translocating step (by similarity).

```
CC -1- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC (methylthio)ethanesulfonate.
CC -1- COFACTOR: Binds 5'-hydroxybenzimidazole]-cobamide as a prosthetic
CC group (By similarity).
CC -1- PATHWAY: Methanogenesis from carbon dioxide; sixth step.
CC -1- SUBUNIT: The complex is composed of 8 subunits; mtrA, mtrB, mtrC,
CC mtrD, mtrE, mtrF, mtrG and mtrH (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane-anchored (By similarity).
CC -1- SIMILARITY: Belongs to the mtrA family.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: A6010686; AAM03725.1; -.
CC HAMAP: MF_01093; -.
CC DR InterPro: IPR005778; Met_transA.
CC DR Pfam: PF04208; MtrA; 1.
CC DR TIGRPFAMs: TIGR01111; mtrA; 1.
CC KM Cobalt; Complete proteome; Methanogenesis; Methyltransferase;
CC One-carbon metabolism; Transmembrane.
CC FT DOMAIN 1 218 Cytoplasmic (Potential).
CC TRANSMEM 219 239 Potential.
CC FT DOMAIN 240 240 Extracellular (Potential).
CC FT DOMAIN 169 176 Poly-Glu.
CC FT DOMAIN 232 238 Poly-Leu.
CC FT BINDING 85 85 5'-hydroxybenzimidazole]-cobamide
CC cofactor (By similarity).
CC SQ SEQUENCE 240 AA; 25342 MW; 86D81A2B358D2079 CRC64;

Query Match 2.5%; Score 8; DB 1; Length 240;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ILGLLLIG 11
Db 232 ILGLLLIG 239

RESULT 14
MTR_A METBA STANDARD; PRT; 240 AA.
ID MTR_A METBA STANDARD; PRT; 240 AA.
AC Q9Y8K4;
DT 29-MAR-2004 (Rel. 43, Created)
DT 03-JUL-2004 (Rel. 43, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Tetrahydromethanopterin S-methyltransferase subunit A (EC 2.1.1.86)
DE (NS-methyltetrahydromethanopterin--coenzyme M methyltransferase
DE subunit A).
GN Name:mtrA;
OS Methanosarcina barkeri.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Puaro / DSM 804;
RX MEDLINE=99268446; PubMed=10338124;
RA Hippler B., Thauer R.K.;
RT "The energy conserving methyltetrahydromethanopterin:coenzyme M
RT methyltransferase complex from methanogenic archaea: function of the
RT subunit MtrH."
RT FEBS Lett. 449:165-168(1999).
RL -1- FUNCTION: Part of a complex that catalyzes the formation of
CC methyl-coenzyme M and tetrahydromethanopterin from coenzyme M and
CC methyl-tetrahydromethanopterin. This is an energy-conserving,
CC sodium-ion translocating step (By similarity).
CC -1- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
```

```
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC (methylthio)ethanesulfonate.
CC -1- COFACTOR: Binds 5'-hydroxybenzimidazole]-cobamide as a prosthetic
CC group (By similarity).
CC -1- PATHWAY: Methanogenesis from carbon dioxide; sixth step.
CC -1- SUBUNIT: The complex is composed of 8 subunits; mtrA, mtrB, mtrC,
CC mtrD, mtrE, mtrF, mtrG and mtrH (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane-anchored (By similarity).
CC -1- SIMILARITY: Belongs to the mtrA family.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AJ132817; CAB41642.1; -.
CC HAMAP: MF_01093; -.
CC DR InterPro: IPR005778; Met_transA.
CC DR Pfam: PF04208; MtrA; 1.
CC DR TIGRPFAMs: TIGR01111; mtrA; 1.
CC KM Cobalt; Methanogenesis; Methyltransferase; One-carbon metabolism;
CC Transmembrane.
CC FT DOMAIN 1 218 Cytoplasmic (Potential).
CC TRANSMEM 219 239 Potential.
CC FT DOMAIN 240 240 Extracellular (Potential).
CC FT DOMAIN 169 176 Poly-Glu.
CC FT DOMAIN 232 238 Poly-Leu.
CC FT BINDING 85 85 5'-hydroxybenzimidazole]-cobamide
CC cofactor (By similarity).
CC SQ SEQUENCE 240 AA; 25413 MW; A3D04EB09F6AD344 CRC64;

Query Match 2.5%; Score 8; DB 1; Length 240;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ILGLLLIG 11
Db 232 ILGLLLIG 239

RESULT 15
MTR_A METBA STANDARD; PRT; 240 AA.
ID MTR_A METBA STANDARD; PRT; 240 AA.
AC O59640;
DT 15-JUL-1999 (Rel. 38, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tetrahydromethanopterin S-methyltransferase subunit A (EC 2.1.1.86)
DE (NS-methyltetrahydromethanopterin--coenzyme M methyltransferase
DE subunit A).
GN Name:mtrA; Ordered locus names=MM1543;
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=98218550; PubMed=9559648;
RA Lienard T., Gottschalk G.;
RT "Cloning, sequencing and expression of the genes encoding the sodium
RT translocating NS-methyltetrahydromethanopterin:coenzyme M
RT methyltransferase of the methylotrophic archaeon Methanosarcina mazei
RT Goel."
RT FEBS Lett. 425:204-208(1998).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=1215824;
RA Depmeijer U., Johann A., Hartoch T., Meckl R., Schmitz R.A.,
```

RA Martinez-Arias R., Henne A., Wlezer A., Baumer S., Jacob C.,
 RA Bruggemann H., Lienard T., Christmann A., Bomecke M., Steckel S.,
 RA Bhattacharyya A., Lykide A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
 RA Fritz H.-J., Gottschalk G.,
 RT The genome of *Methanocaldococcus jassbyi*: evidence for lateral gene
 transfer between Bacteria and Archaea.
 RL J. Mol. Microbiol. Biotechnol. 4:453-461 (2002).
 CC -1- FUNCTION: Part of a complex that catalyzes the formation of
 methyl-coenzyme M and tetrahydromethanopterin from coenzyme M and
 methyl-tetrahydromethanopterin. This is an energy-conserving,
 sodium-ion translocating step.
 CC CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
 mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
 (methylthio)ethanesulfonate.
 CC -1- COFACTOR: Binds 5'-hydroxybenzimidazole-cobamide as a prosthetic
 group.
 CC -1- PATHWAY: Methanogenesis from carbon dioxide; sixth step.
 CC -1- SUBUNIT: The complex is composed of 8 subunits; mtrA, mtrB, mtrC,
 mtrD, mtrE, mtrF, mtrG and mtrH (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane-anchored (By similarity).
 CC -1- SIMILARITY: Belongs to the mtrA family.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 or send an email to license@ebi.ac.uk).

 CC EMBL; AF042381; AAC38334.1; -.
 DR EMBL; AE013388; AAM31239.1; -.
 DR HAMAP; MF_01093; -1.
 DR InterPro: IPR005778; Met_transa.
 DR Pfam; PF04208; MtrA; 1.
 DR TIGR/Pfam; TIGR01111; mtrA; 1.
 KW Cobalt; Complete proteome; Methanogenesis; Methyltransferase;
 KM One-carbon metabolism; Transferase; Transmembrane.
 FT DOMAIN 1 218 Cytoplasmic (Potential).
 FT TRANSMEM 219 239 Potential.
 FT DOMAIN 240 240 Extracellular (Potential).
 FT DOMAIN 169 176 Poly-Glu.
 FT BINDING 85 5'-hydroxybenzimidazole-cobamide
 cofactor (By similarity).
 FT FT CONFLICT 16 16 G -> R (in Ref. 1).
 FT CONFLICT 71 71 N -> D (in Ref. 1).
 FT CONFLICT 127 127 E -> G (in Ref. 1).
 FT CONFLICT 161 161 D -> E (in Ref. 1).
 SQ SEQUENCE 240 AA; 25366 MW; 44C086DD3561E526 CRC64;

Query Match 2.5%; Score 8; DB 1; Length 240;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLLG 11
 DB 232 LGGLLLG 239

RESULT 16
 Q6XPV4 PRELIMINARY; PRT; 249 AA.
 AC Q6XPV4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-NOV-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-OCT-2004 (TrEMBLrel. 27, Last annotation update)
 OS Transmembrane receptor PEGMARIII-X.
 DE Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A.

RA Teusner J.T., Belford D.A., Powell B.C.,
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY219230; AAP44530.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PR00047; Ig_2.
 DR SMART; SM00409; Ig_2.
 DR SMART; SM00408; Ig_c2; 2.
 DR PROSITE; PS50835; Ig_LIKE; 2.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 249 AA; 28168 MW; C58B6B2B97595D21 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 ADSGSYFC 211
 DB 164 ADSGSYFC 171

RESULT 17
 AAP44530 PRELIMINARY; PRT; 249 AA.
 AC AAP44530;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 OS Transmembrane receptor PEGMARIII-X.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RA Teusner J.T., Belford D.A., Powell B.C.,
 RT Identification of a novel rat receptor homologous to human
 PEGMARIII-A.
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY219230; AAP44530.1; -.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 249 AA; 28168 MW; C58B6B2B97595D21 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 ADSGSYFC 211
 DB 164 ADSGSYFC 171

RESULT 18
 Q46648 PRELIMINARY; PRT; 265 AA.
 AC Q46648;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE HrcT.
 GN Name=hrcT;
 OS *Erwinia amylovora*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Erwinia*.
 OC NCBI_TaxID=552;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=521;
 RX MEDLINE=96198177; PubMed=8626302;
 RA Bogdanove A.J., Wei Z.M., Zhao L., Beer S.V.;

```

RT "Brwnia amylovora secretes harpin via a type III pathway and contains
a homolog of yopN of Yersinia spp.";
RL J. Bacteriol. 178:1720-1730(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL: L25828; AAB06007.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0006605; P:protein targeting; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR006304; SPAR_Yact.
DR InterPro: IPR002010; TYPE3IMPRPROT.
DR Pfam: PF01311; Bac_export_1; 1.
DR PRINTS: PR00953; TYPE3IMPRPROT.
DR TIGRFAMs: TIGR01401; flir_like_III; 1.
KM Tmembrane.
SQ SEQUENCE 265 AA; 28988 MW; C3B85FD87ECC23D2 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILGLLL 9
DB 83 GILGLLL 90

RESULT 19
Q95KP8 PRELIMINARY; PRT; 269 AA.
AC Q95KP8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sialic acid-binding lectin Siglec-L1 (Fragment).
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX NCBI_Taxid=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21523976; PubMed=11546777;
RA Angata T., Varki N.M., Varki A.;
RT "A second uniquely human mutation affecting sialic acid biology.";
RL J. Biol. Chem. 276:40282-40287(2001).
DR EMBL: AY029757; AAKS0564.1; -.
DR HSP: Q9Y286; 107S.
DR GO: GO:0005529; F:sugar binding; IEA.
DR GO: GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro: IPR003599; IG_1like.
DR InterPro: IPR007110; IG_1like.
DR Pfam: PF00047; IG_1.
DR SMART: SM00409; IG_2.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Lectin.
FT NON TER 269
SQ SEQUENCE 269 AA; 30649 MW; D1277346EC3C7CA CRC64;

Query Match 2.5%; Score 8; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LEVPESVT 30
DB 153 LEVPESVT 160

RESULT 20
Q95KP9 PRELIMINARY; PRT; 269 AA.
AC Q95KP9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

```

```

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sialic acid-binding lectin Siglec-L1 (Fragment).
OS Gorilla gorilla (Gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_Taxid=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21523976; PubMed=11546777;
RA Angata T., Varki N.M., Varki A.;
RT "A second uniquely human mutation affecting sialic acid biology.";
RL J. Biol. Chem. 276:40282-40287(2001).
DR EMBL: AY029754; AAKS0563.1; -.
DR HSP: Q9Y286; 107S.
DR GO: GO:0005529; F:sugar binding; IEA.
DR GO: GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro: IPR003599; IG_1like.
DR InterPro: IPR007110; IG_1like.
DR Pfam: PF00047; IG_1.
DR SMART: SM00409; IG_2.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Lectin.
FT NON TER 271
SQ SEQUENCE 271 AA; 30613 MW; F63B6018C1C7B934 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LEVPESVT 30
DB 153 LEVPESVT 160

RESULT 21
Q95KQ0 PRELIMINARY; PRT; 271 AA.
AC Q95KQ0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sialic acid-binding lectin Siglec-L1 (Fragment).
OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_Taxid=9597;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21523976; PubMed=11546777;
RA Angata T., Varki N.M., Varki A.;
RT "A second uniquely human mutation affecting sialic acid biology.";
RL J. Biol. Chem. 276:40282-40287(2001).
DR EMBL: AY029753; AAKS0562.1; -.
DR HSP: Q9Y286; 107S.
DR GO: GO:0005529; F:sugar binding; IEA.
DR GO: GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro: IPR003599; IG_1like.
DR InterPro: IPR007110; IG_1like.
DR Pfam: PF00047; IG_1.
DR SMART: SM00409; IG_2.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Lectin.
FT NON TER 271
SQ SEQUENCE 271 AA; 30613 MW; F63B6018C1C7B934 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LEVPESVT 30
DB 153 LEVPESVT 160

```


Db 155 LEVPESVT 162

RESULT 22

Q6SFH9 PRELIMINARY; PRT; 292 AA.
ID Q6SFH9
AC Q6SFH9;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Membrane protein, putative.
GN ORFNames=EBAC000-36A07.83;
OS uncultured bacterium 580.
OC Bacteria; environmental samples.
OX NCBI_TaxID=257400;
RN [1]
RP SEQUENCE FROM N.A.
RA DeLong E.F.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Heidelberg J.F., Bisen J.A., Nelson W.C., DeLong E.F.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ458647; AAR38238.1; -.
DR InterPro; IPR000620; DUF6.
DR Pfam; PF00892; DUF6; 2.
SQ SEQUENCE 292 AA; 32975 MW; E3A21B8F5B89D14 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILGLLL 10
Db 277 ILGLLL 284

RESULT 23

AAR38238 PRELIMINARY; PRT; 292 AA.
ID AAR38238
AC AAR38238;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DE Membrane protein, putative.
GN EBAC000-36A07.83.
OS uncultured bacterium 580.
OC Bacteria; environmental samples.
OX NCBI_TaxID=257400;
RN [1]
RP SEQUENCE FROM N.A.
RA DeLong E.F.;
RL "Monterey Bay Coastal Ocean Microbial Observatory environmental clone sequencing."
RT Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Heidelberg J.F., Bisen J.A., Nelson W.C., DeLong E.F.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ458647; AAR38238.1; -.
SQ SEQUENCE 292 AA; 32975 MW; E3A21B8F5B89D14 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILGLLL 10
Db 277 ILGLLL 284

RESULT 24

ID Q702H2 PRELIMINARY; PRT; 346 AA.
AC Q702H2;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Organic anion transporter 2 (Fragment).
GN Name=oa2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Geyer J., Petzinger E.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AF627253; CAF28454.1; -.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub transporter.
DR Pfam; PF00083; Sugar tr; 1.
DR PROSITE; PS50850; MFS; 1.
KW Transmembrane.
FT NON TER 1
FT NON TER 346
SQ SEQUENCE 346 AA; 38394 MW; 96508FAD632FE096 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 291 ISLCMVV 298
Db 231 ISLCMVV 238

RESULT 25

CAF28454 PRELIMINARY; PRT; 346 AA.
ID CAF28454
AC CAF28454;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DE Organic anion transporter 2 (Fragment).
GN OAT2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Geyer J., Petzinger E.;
RL "Cloning of the organic anion transporter Oat2 from bovine kidney."
RT Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ627253; CAF28454.1; -.
FT NON TER 1
FT NON TER 346
SQ SEQUENCE 346 AA; 38394 MW; 96508FAD632FE096 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 291 ISLCMVV 298
Db 231 ISLCMVV 238

RESULT 26

Q9GJEB


```

ID 09GJ33 PRELIMINARY; PRT; 350 AA.
AC 09GJ33;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE MHC class I antigen.
GN Name=Mamc-I;
OS Mamota monax (woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuriidae; Scuriinae;
OC Mamota.
OC NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang D.-L., Zhou J.-H., Lu M., Gross-Wild H., Rogendorf M.;
RT "There are at least two loci in woodchuck MHC class I gene.";
RL Tissue Antigens 0:0-0(2000).
DR EMBL/ AF201912; AAC3957.1; -.
DR HSSP; Q2961; IHS.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; IG-1ike.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF07654; CI-sect; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PRO1638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGL; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR KEGG; K00000; MHC_I; 1.
SQ SEQUENCE 350 AA; 40772 MW; 629E9B7BDP8472P1 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILGILL 9
DB 307 GILGILL 314

RESULT 27
Q6TV6 PRELIMINARY; PRT; 366 AA.
AC Q6TV6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE 57L.
OS Yaba monkey tumor virus (YMTV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Yatapoxvirus.
OC NCBI_TaxID=38804;
RN [1]
RP SEQUENCE FROM N.A.
RA Brunetti C.R., Paulose-Murphy M., Singh R., Qin J., Barrett J.W.,
RA Tardivel A., Schneider P., Essani K., McFadden G.;
RT "A secreted high-affinity inhibitor of human TNF from Tanapox virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4831-4836(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=95248279; PubMed=7730796;
RA Amano H., Ueda Y., Miyamura T.;
RT "Identification and characterization of the thymidine kinase gene of
RT Yaba virus.";
RL J. Gen. Virol. 76:1109-1115(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=14645589;

```

```

RA Brunetti C.R., Amano H., Ueda Y., Qin J., Miyamura T., Suzuki T.,
RA Li X., Barrett J.W., McFadden G.;
RT "Complete genomic sequence and comparative analysis of the tumorigenic
RT poxvirus Yaba monkey tumor virus.";
RL J. Virol. 77:13335-13347(2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Brunetti C.R., Paulose-Murphy M., Singh R., Qin J., Barrett J.W.,
RA Tardivel A., Schneider P., Essani K., McFadden G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY386371; AAR07413.1; -.
DR InterPro; IPR008787; Pox_G7.
DR Pfam; PF05503; Pox_G7; 1.
SQ SEQUENCE 366 AA; 41961 MW; 3B8F0CDE2053A82F CRC64;

Query Match 2.5%; Score 8; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 VATLSTLL 197
DB 116 VATLSTLL 123

RESULT 28
AAR07413 PRELIMINARY; PRT; 366 AA.
AC AAR07413;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE 57L.
OS Yaba monkey tumor virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Yatapoxvirus.
OC NCBI_TaxID=38804;
RN [1]
RP SEQUENCE FROM N.A.
RA Brunetti C.R., Amano H., Ueda Y., Qin J., Miyamura T., Suzuki T.,
RA Li X., Barrett J.W., McFadden G.;
RT "Identification and characterization of the thymidine kinase gene of
RT Yaba virus.";
RL J. Gen. Virol. 76:1109-1115(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Brunetti C.R., Amano H., Ueda Y., Qin J., Miyamura T., Suzuki T.,
RA Li X., Barrett J.W., McFadden G.;
RT "Complete Genomic Sequence and Comparative Analysis of the Tumorigenic
RT poxvirus Yaba Monkey Tumor Virus.";
RL J. Virol. 77:13335-13347(2003).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22584400; PubMed=12676996;
RA Brunetti C.R., Paulose-Murphy M., Singh R., Qin J., Barrett J.W.,
RA Tardivel A., Schneider P., Essani K., McFadden G.;
RT "A secreted high-affinity inhibitor of human TNF from Tanapox virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4831-4836(2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Brunetti C.R., Paulose-Murphy M., Singh R., Qin J., Barrett J.W.,
RA Tardivel A., Schneider P., Essani K., McFadden G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY386371; AAR07413.1; -.
SQ SEQUENCE 366 AA; 41961 MW; 3B8F0CDE2053A82F CRC64;

Query Match 2.5%; Score 8; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 VATLSTLL 197
DB 116 VATLSTLL 123

```

```

RESULT 29
ID 030187 PRELIMINARY; PRT; 412 AA.
AC 030187;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein AF0049.
OS OrderedLocustNames=AF0049;
OC Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwin M.L., Hickey E.K., Peterson J.D.,
RA Reichmann D.L., Krelavague A.R., Graham D.E., Kyriades N.C.,
RA Kirchess E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
RA Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodok A.,
RA Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A.,
RA Utecherback T.R., Cotton M.D., Spriggs T., Artlach P., Kaine B.P.,
RA Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
RA Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
RA Moese C.R., Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
DR EMBL; AE001103; AAB91183.1; -.
DR PIR; A69256; A69256.
DR TIGR; AF0049; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 412 AA; 45909 MW; 6A23FBF73640E310 CRC64;

Query Match 2.5% Score 8; DB 2; Length 412;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 YIGETSAG 277
|||
Db 142 YIGETSAG 149

RESULT 30
PSL2 HUMAN STANDARD; PRT; 520 AA.
ID 08TCB8; O8TAW1; O96S28;
AC 08TCB8; O8TAW1; O96S28;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Signal peptide peptidase-like 2A (BC 3.4.99.-) (SPP-1like 2A protein)
DE (SPP1za protease) (intramembrane protease 3) (IMP3) (Presentin-1like
DE protein 2).
GN Name=SPP1za; Synonyms=PSL2;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RC Irmeler M., Tomiuk S., Korner M.R., Hofmann K., Conradt M.;
RT "Characterization of a new protein family with homology to
RT presentin-1."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22135308; PubMed=12139484;
RA Grigorenko A.P., Moliaka Y.K., Korovaitseva G.I., Rogaev E.I.;

```

```

RT "Novel class of polycyclic proteins with domains associated with
RT putative protease activity."
RL Biokhimiia 67:826-834(2002).
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Oca T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Pancereas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Uedlin T.B., Toshlyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren S.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton B., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield J.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
RP SEQUENCE OF 91-520 FROM N.A.
RC TISSUE=Teratocarcinoma;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa B.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y.,
RA Iehida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiyama S., Komai F., Hara R., Takuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Taniguchi A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Omori Y.,
RA Kawabata A., Hikiji T., Kobatake K., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi K., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
RN
RP SEQUENCE OF 91-520 FROM N.A.
RC TISSUE=Cervical carcinoma;

```

```

RX MEDLINE=22072745; PubMed=12077416; DOI=10.1126/science.1070925;
RA Wehlofen A., Binn K., Lemberg M.K., Ashman K., Martoglio B.;
RT "Identification of signal peptide peptidase, a presenilin-type
RL Science 296:2215-2218 (2002).
CC -1- FUNCTION: May act as intramembrane protease.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: Belongs to the presenilin family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; AJ345028; CAC8789.1; -
DR EMBL; AY169314; AAO12539.1; -
DR EMBL; AK075454; BAC11630.1; -
DR EMBL; BC025740; AAR25740.1; -
DR EMBL; AK027446; BAB5117.1; ALT_INIT.
DR EMBL; AJ420896; CAD1313.1; ALT_INIT.
DR MEROPS; A22.007; -
DR MIM; 608238; -
DR InterPro; IPR003137; PA.
DR InterPro; IPR006639; Peptidase_A22.
DR InterPro; IPR007369; Peptidase_A22B.
DR Pfam; PF02225; PA; 1.
DR Pfam; PF04258; Peptidase_A22B; 1.
DR SMART; SM00730; PSN; 1.
KW Hydrolyase; Protease; Transmembrane.
FT DOMAIN 1 172 Cytoplasmic (Potential).
FT TRANSMEM 173 193 Potential.
FT TRANSMEM 221 241 Potential.
FT TRANSMEM 248 268 Potential.
FT TRANSMEM 286 306 Potential.
FT TRANSMEM 312 332 Potential.
FT TRANSMEM 341 361 Potential.
FT TRANSMEM 400 420 Potential.
FT TRANSMEM 438 458 Potential.
FT TRANSMEM 461 481 Potential.
FT DOMAIN 55 152 PA.
FT CONFLICT 126 126 N -> D (in Ref. 5).
FT CONFLICT 271 271 I -> T (in Ref. 3).
FT CONFLICT 406 406 S -> L (in Ref. 3).
FT CONFLICT 446 446 I -> F (in Ref. 3).
FT CONFLICT 511 511 V -> E (in Ref. 5).
SQ SEQUENCE 520 AA; 58143 MW; A7A933A6504507DC CRC64;

Query Match 2.5%; Score 8; DB 1; Length 520;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILGLLL 10
Db 342 ILGLLL 349

RESULT 31
O7OIRO PRELIMINARY; PRT; 537 AA.
AC O7OIRO;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE AGCP3417 (Fragment).
DE Name=agCS54408; ORFName=ENSANGC00000012635;
OS Anopheles gambiae str. PBST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB0100807; EAA04152.1; -
DR GO; GO:0016758; P:transferase activity, transferring hexosyl . . . ; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002213; UDP_glycosyltrans.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 537 AA; 59693 MW; 5B495D82947DCD1 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 537;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ILGLLL 11
Db 21 ILGLLL 28

RESULT 32
O6BSF5 PRELIMINARY; PRT; 590 AA.
AC O6BSF5;
DT 01-OCT-2004 (Tremblrel. 28, Created)
DT 01-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Similar to Ca1037[CamMS1 Candida albicans CamMS1.
DE ORFName=DEHA0D101539;
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=4959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS8767;
RG GENOMEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul J., Aigle M., Anthouard V., Babour A., Barde V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boistrane A., Boyer J., Cartolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropl A.,
RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.M., Nikolaki M., Ozas S., Ozler-Kalogropoulos O.,
RA Pellenz S., Porter S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Jouvet M., Westhof E., Wirth B.,
RA Zentou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CS8767;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382136; CAC87017.1; -
SQ SEQUENCE 590 AA; 67544 MW; B06BED6770A98228 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 590;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 181 QTNQBP 188

```



```

FT CARBOHYD 385 385 N-linked (GlcNAc...) (Potential)
FT VARSPIC 4 141 LILLPLLCGRVAGKOKXVLTLMQSLVYQELCYSLYC
FT SPSYFQNGWRTASDVHGWYPRAGDHSNIPATNNPAPRAY
FT QETRDHFHLGDSPQNDCTSLIDTESDAGTVFCVERG
FT NMKNVXYDQLSVV -> PLTMANBERSDGMADPRFS
FT (in Isoform Short)
FT /Frtid=VSP_002566
FT P -> T (in dbSNP:2034691).
FT /Frtid=VAR_014259
FT R -> W (in Ref. 3).
SQ SEQUENCE 595 AA; 64984 MW; D05662176274C5C3 CRC64;

Query Match 2.5%; Score 8; DB 1; Length 595;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LEVPESTV 30
DB 153 LEVPESTV 160

RESULT 34
SILL_PANTR STANDARD; PRT; 597 AA.
AC 095LH0;
DT 28-FEB-2003 (Ref. 41, Created)
DT 28-FEB-2003 (Ref. 41, Last sequence update)
DT 01-OCT-2004 (Ref. 45, Last annotation update)
DE Sialic acid binding Ig-1-like lectin-like 1 precursor (Siglec-like molecule 1) (Siglec-L1).
GN Name=SIGLEC1;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21523976; PubMed=11546777; DOI=10.1074/jbc.M105926200;
RA Angata T., Varki N.M., Varki A.;
RT A second uniquely human mutation affecting sialic acid biology.;
RL J. Biol. Chem. 276:40282-40287(2001).
CC -1- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-containing phosphatases.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (sialic acid binding Ig-1-like lectin) family.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements or send an email to license@ebi.ac.uk).

```

```

FT SIGNAL 1 20 Potential.
FT CHAIN 21 597 Sialic acid binding Ig-1-like lectin-like 1.
FT 095LH0; Extracellular (Potential).
FT DOMAIN 21 483 Potential.
FT TRANSMEM 484 504 Cytoplasmic (Potential).
FT DOMAIN 505 597 Ig-1-like V-type 1.
FT DOMAIN 21 144 Ig-1-like V-type 2.
FT DOMAIN 145 271 Ig-1-like C2-type 1.
FT DOMAIN 277 360 Ig-1-like C2-type 2.
FT DOMAIN 367 464 Ig-1-like C2-type 2.
FT SITE 565 570 ITIM motif.
FT SITE 588 593 SLAM-LIKE MOTIF.
FT DISULFID 46 106 By similarity.
FT DISULFID 168 301 By similarity.
FT DISULFID 173 233 By similarity.
FT DISULFID 295 344 By similarity.
FT DISULFID 403 448 By similarity.
FT CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 181 181 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 232 232 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 362 362 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 369 369 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 387 387 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 597 AA; 65075 MW; 74C13CFA9CDB5B85 CRC64;

Query Match 2.5%; Score 8; DB 1; Length 597;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LEVPESTV 30
DB 155 LEVPESTV 162

RESULT 35
06IBL2
ID 06IBL2 PRELIMINARY; PRT; 612 AA.
AC 06IBL2;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE OS-9 protein.
GN Name=OS-9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ebert L., Schlick W., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CRA56791; CAG33072.1; -
DR InterPro; IPR009011; Man6php_recept.
SQ SEQUENCE 612 AA; 69232 MW; FC6854FFB1B26SD CRC64;

Query Match 2.5%; Score 8; DB 2; Length 612;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGULLLG 11
DB 10 LIGULLLG 17

RESULT 36
09BW99
ID 09BW99 PRELIMINARY; PRT; 612 AA.
AC 09BW99; Q81Z58;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE OS-9 protein.

```

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toobyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
RA Krzyvinski M.I., Skalka U., Smallus D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC000532; AA00532.1; -.
DR EMBL; BC007254; AA07254.1; -.
DR EMBL; BC023513; AA023513.2; -.
DR InterPro; IPR009011; Man5chp_Recept.
SQ SEQUENCE 612 AA; 69246 MW; 1FD06F7B23101015 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 612;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILLG 11
DB 10 LIGLILLG 17

RESULT 37
CAG33072 PRELIMINARY; PRT; 612 AA.
AC CAG33072;
DT 01-JUN-2004 (TREMBlrel. 27, Created)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 01-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE OS-9 protein.
OS OS-9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry
vector (pDONR201).";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR456791; CAG33072.1; -.
SQ SEQUENCE 612 AA; 69232 MW; FC6854FEF11B26BD CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 612;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILLG 11
DB 10 LIGLILLG 17

RESULT 38
C6JH13 PRELIMINARY; PRT; 655 AA.
AC C6JH13;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Thrombospondin-related anonymous protein.
GN Name=trap;
OS Babesia bovis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=5865;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Israel C61411;
RX PubMed=15138064;
RA Gaffar F.R., Yatsuda A.P., Franssen F.F., Vries Ed B.;
RT "A Babesia bovis merozoite protein with a domain architecture highly
similar to the thrombospondin-related anonymous protein (TRAP) present
in Plasmodium sporozoites.";
RL Mol. Biochem. Parasitol. 136:25-34(2004).
DR EMBL; AY486102; AAS58046.1; -.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF000092; VWA_1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFPA; 1.
SQ SEQUENCE 655 AA; 71322 MW; 4FF6306B480BD3F5 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 655;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILLG 11
DB 595 LIGLILLG 602

RESULT 39
AAS58046 PRELIMINARY; PRT; 655 AA.
AC AAS58046;
DT 01-JUN-2004 (TREMBlrel. 27, Created)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 01-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE Thrombospondin-related anonymous protein.
GN TRAP.
OS Babesia bovis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=5865;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Israel C61411;
RX PubMed=15138064;
RA Gaffar F.R., Yatsuda A.P., Franssen F.F., Vries Ed B.;
RT "A Babesia bovis merozoite protein with a domain architecture highly
similar to the thrombospondin-related anonymous protein (TRAP) present

```

```

RT      in Plasmodium sporozoites.",
RL      Mol. Biochem. Parasitol. 136:25-34 (2004).
DR      EMBL; AY486102; AAS58046.1; -.
SQ      SEQUENCE      655 AA; 71322 MW; 4FF6306B4806DF5 CRC64;

Query Match      2.5%; Score 8; DB 2; Length 655;
Best Local Similarity 100.0%; Pred. No. 71;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      4 LAGLLLLG 11
        |||||
Db      595 LIGLLLLG 602

RESULT 40
ID      OS9_HUMAN      STANDARD; PRT; 667 AA.
AC      Q13438; O00579;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Protein OS-9 precursor.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96198566; Pubmed=8634085;
RA      Su Y.A., Hutter C.M., Trent U.M., Meltzer P.S.;
RT      "Complete sequence analysis of a gene (OS-9) ubiquitously expressed in
RT      human tissues and amplified in sarcomas.";
RL      Mol. Carcinog. 15:270-275(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98158329; Pubmed=9498564;
RA      Kimura Y., Nakazawa M., Tsuchiya N., Asakawa S., Shimizu N.,
RA      Yamada M.;
RT      "Genomic organization of the OS-9 gene amplified in human sarcomas.";
RL      J. Biochem. 122:1190-1195(1997).
RN      [3]
RP      SEQUENCE FROM N.A., CHARACTERIZATION, AND ALTERNATIVE PRODUCTS.
RC      TISSUE=Promyelocytic leukemia;
RX      MEDLINE=98230694; Pubmed=9562620;
RA      Kimura Y., Nakazawa M., Yamada M.;
RT      "Cloning and characterization of three isoforms of OS-9 cDNA and
RT      expression of the OS-9 gene in various human tumor cell lines.";
RL      J. Biochem. 123:876-882(1998).
RN      [4]
RP      SEQUENCE OF 194-667 FROM N.A.
RX      MEDLINE=97336055; Pubmed=9192650;
RA      Elkhilouni A.G., Krizman D.B., Wang Z., Hofmann T.A., Roe B.,
RA      Meltzer P.S.;
RT      "Transcript mapping in a 46-kb sequenced region at the core of 12q13.3
RT      amplification in human cancers.";
RL      Genomics 42:295-301(1997).
CC      -1- FUNCTION: May play a role in cell viability.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=3;
CC      Name=OS-9-1;
CC      IsoId=Q13438-1; Sequence=Displayed;
CC      Name=OS-9-2;
CC      IsoId=Q13438-2; Sequence=VSP_004353;
CC      Name=OS-9-3;
CC      IsoId=Q13438-3; Sequence=VSP_004352, VSP_004353;
CC      -1- TISSUE SPECIFICITY: Ubiquitously expressed. Found as well in all
CC      tumor cell lines analyzed, amplified in sarcomas. Highly expressed
CC      in osteosarcoma OSA-CI and rhabdomyosarcoma RH30 cell lines. OS-9-
CC      2 is the major isoform detected in all cell types examined.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -

```

CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use by non-profit institutions as long as its content is in no way
CC		modified and this statement is not removed. Usage by and for commercial
CC		entities requires a license agreement (See http://www.ebi.ac.uk/ncbi/entrez/) or send an email to license@ebi.ac.uk .
CC		-----
DR	EMBL, U41635; AAB06495.1; -.	
DR	EMBL, AB002805; BAA24362.1; -.	
DR	EMBL, AB002806; BAA24363.1; -.	
DR	EMBL, U81031; AAC39523.2; -.	
DR	PIR, JCS889; JCS889.	
DR	GO, GO:0005625; C:soluble fraction; TAS.	
DR	GO, GO:0008151; P:cell growth and/or maintenance; TAS.	
DR	InterPro, IPR009011; Man6php_recept.	
KW	Alternative splicing; Polymorphism; Signal.	
FT	SIGNAL	1 25
FT	CHAIN	26 667
FT	DOMAIN	414 429
FT	CARBONHD	177 177
FT	VARSPLIC	456 470
FT		
FT	VARSPLIC	535 589
FT		
FT		/FtId=VSP_004353.
FT	VARIA NT	398 398 R-> W (in dBSNP:1804598).
FT		/FtId=VAR_011897.
FT		
SO	SEQUENCE	667 AA; 75561 MW; 65BAJF66CEC8756 CRC64;
	Query Match	2.5%; Score 8; DB 1; Length 667;
	Best Local Similarity	100.0%; Pred. NO. 72;
	Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	4 LLGLLLG 11 10 LLGLLLG 17	
Db		
RESULT 41		
ID	Q7ZTS9	PRELIMINARY; PTR; 750 AA.
AC	Q7ZTS9	
DT	05-JUL-2004 (TREMBLrel. 27, Created)	
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TREMBLrel. 27, last annotation update)	
DE	ATP-dependent RNA helicase.	
CN	OrderedLocustNames=LIC10938;	
OS	Leptosira interrogans (betagroup Icterohaemorrhagiae / serovar Copenhagen1).	
OC	Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.	
OX	NCBI_TaxID=44275;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Flecuruz LI-130;	
RX	PubMed=15028702;	
RA	Nasacimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,	
RA	Ho P.L., Haake D.A., Verjovski-Almeida S., Hartsbeek R.A.,	
RA	Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,	
RA	Continho L.L., Degraev W.M., Dellagostin O.A., El-Dorri H.,	
RA	Ferreto B.S., Ferro M.I.T., Furlan L.R., Gambellini M., Gigliotti E.A.,	
RA	Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,	
RA	Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,	
RA	Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,	
RA	de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,	
RA	Siqueira W.J., Sommer P., Tsai S.M., Simpson A.U.G., Ferro J.A.,	
RA	Camargo L.E.A., Kitzajima J.P., Setubal J.C., Van Slyke M.A.,	
RT	"Comparative genomics of two Leptospira interrogans serovars reveals	
RL	novel insights into physiology and pathogenesis.";	
RU	J. Bacteriol. 186:2164-2172(2004).	
DR	EMBL; AE017290; AAS69549.1; -.	
DR	GO, GO:0004386; P:helicase activity; IEA.	
DR	InterPro, IPR006474; Cas3_core.	
DR	InterPro, IPR011545; DEAD/DEAF_N.	
DR	InterPro, IPR001650; Helicase_C.	


```

DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00490; HelicC; 1.
DR TIGRPFAM; TIGR01587; Cae3_core; 1.
KW Complete proteome; Helicase.
SQ SEQUENCE 750 AA; 84879 MW; B075B49FA0EDBCB7 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 KSLPVPFAL 287
Db 555 KSLPVPFAL 562

RESULT 42
AAS69549 PRELIMINARY; PRT; 750 AA.
ID AAS69549;
AC AAS69549;
DT 24-MAR-2004 (TrEMBLrel. 27, Created)
DT 24-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE ATP-dependent RNA helicase.
GN IIC10938.
OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar Copenhageni).
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
NC NCB1_TaxID=44275;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Flacruz L1-130;
RX PubMed=15028702;
RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorcello C.B.,
RA Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeel R.A.,
RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carter H.,
RA Coutinho L.B., Degraeve W.M., Dellagostin O.A., El-Dorri H.,
RA Perro E.S., Ferro M.I.T., Furlan L.R., Gambellini M., Gagliocci E.A.,
RA Goes-Neto A., Goldman G.H., Goldman M.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo J.L.M., Kimura E.T.,
RA Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schrieler A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172(2004).
DR EMBL; AEO17290; AAS69549.1; -.
KW Helicase.
SQ SEQUENCE 750 AA; 84879 MW; B075B49FA0EDBCB7 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 KSLPVPFAL 287
Db 555 KSLPVPFAL 562

RESULT 43
Q8F1E6 PRELIMINARY; PRT; 752 AA.
ID Q8F1E6;
AC Q8F1E6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ATP-dependent RNA helicase, putative.
GN Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
NC NCB1_TaxID=173;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint-Gilons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AEO11481; AAN50388.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR006474; Cae3_core.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HelicC; 1.
DR TIGRPFAM; TIGR01587; Cae3_core; 1.
KW ATP-binding; Complete proteome; Helicase; Hydrolase.
SQ SEQUENCE 752 AA; 85093 MW; 2B71EF572385C0E CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 KSLPVPFAL 287
Db 555 KSLPVPFAL 562

RESULT 44
Q86AH2 PRELIMINARY; PRT; 937 AA.
ID Q86AH2;
AC Q86AH2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to Dictyostellium discoideum (Slime mold).
DE kDa protein.
OS Dictyostellium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidida; Dictyostelium.
NC NCB1_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szafranski K., Pachbat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Nogel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostellium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC115599; AAO51504.1; -.
DR InterPro; IPR008615; FNIP.
DR Pfam; PF05725; FNIP; 4.
KW Hypothetical protein.
SQ SEQUENCE 937 AA; 105880 MW; BEC2FEA936489778 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 99;

```


Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 123 NOVVRDKI 130
 |||||
 Db 115 NOVVRDKI 122

RESULT 45

CHRD_MOUSE STANDARD; PRT; 948 AA.

AC Q920E2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chordin precursor.
 GN Name=Chrd;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6SJL/F1;
 RA Lu B., Bachiller D., Agius E., Piccolo S., De Robertis E.M.;
 RT "BMP-binding domains in the chordin secreted protein."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

SEQUENCE FROM N.A.
 MEDLINE=99000848; PubMed=9782094;
 RA Pappano W.N., Scott I.C., Clark T.G., Eddy R.L., Shows T.B.,
 RA Greenspan D.S.;
 RT "Coding sequence and expression patterns of mouse chordin and mapping
 of the cognate mouse chrd and human CHRD genes."
 RL Genomics 52:236-239(1998).
 CC -1- FUNCTION: Dorsalizing factor. Key developmental protein that
 dorsalizes early vertebrate embryonic tissues by binding to
 ventralizing TGF-beta family bone morphogenetic proteins (BMPs)
 and sequestering them in latent complexes.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- DEVELOPMENTAL STAGE: Detected at high levels of a in 7 dpc mouse
 embryos; its level decrease at later developmental stages and in
 adult tissues.
 CC -1- SIMILARITY: Belongs to the chordin family.
 CC -1- SIMILARITY: Contains 4 CHRD domains.
 CC -1- SIMILARITY: Contains 4 VMP_C domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 or send an email to license@ebi.ac.uk).

EMBL; AF096276; AAC19895.1; -
 EMBL; AF096501; AAC68867.1; -
 DR MGD; MGI:1313268; Chrd.
 DR GO; GO:0007420; P:brain development; IMP.
 DR GO; GO:0009953; P:dorsal/ventral pattern formation; IMP.
 DR GO; GO:0010003; P:gastrointestinal system development; IMP.
 DR GO; GO:0001501; P:skeletal development; IMP.
 DR InterPro; IPR010895; CHRD.
 DR InterPro; IPR006559; SOG.
 DR InterPro; IPR01007; VMP_C.
 DR Pfam; PF07452; CHRD; 4.
 DR Pfam; PF00093; VMC; 4.
 DR SMART; SM00566; SOG; 3.
 DR SMART; SM00214; VMC; 4.
 DR PROSITE; PS50933; CHRD; 4.
 DR PROSITE; PS501208; VMC_1; 2.
 DR PROSITE; PS50184; VMC_2; 2.
 KW Developmental protein; Glycoprotein; Repeat; signal.
 FT SIGNAL 1 26 Potential.

FT CHAIN 27 948 Chordin.
 FT DOMAIN 49 126 VMP_C 1.
 FT DOMAIN 168 277 CHRD 1.
 FT DOMAIN 279 398 CHRD 2.
 FT DOMAIN 399 520 CHRD 3.
 FT DOMAIN 526 646 CHRD 4.
 FT DOMAIN 699 759 VMP_C 2.
 FT DOMAIN 779 845 VMP_C 3.
 FT DOMAIN 867 927 VMP_C 4.
 FT CARBOHYD 347 347 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 430 430 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 877 877 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 948 AA; 101512 MW; 4DC2DA01D9BD2147 CRC64;

Query Match 2.5%; Score 8; DB 1; Length 948;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LLSGLLGG 11
 |||||
 Db 13 LLSGLLGG 20

RESULT 46

OGUW83 PRELIMINARY; PRT; 954 AA.

ID OGUW83;
 AC OGUW83;
 DT 05-JUL-2004 (TREMURel. 27, Created)
 DT 05-JUL-2004 (TREMURel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMURel. 27, Last annotation update)
 DE Chordin.
 GN ORFNames=UNQ217;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Balwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Batton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heide S.,
 RA Huang L., Kim H.S., Kijowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vanden R., Watanabe C., Wileand D., Woods K., Xie M.H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment."
 RT Genome Res. 13:2265-2270(2003).
 RL EMBL; AY358926; AA089285.1; -
 DR InterPro; IPR010895; CHRD.
 DR InterPro; IPR009041; BMP_SGCT.
 DR InterPro; IPR006559; SOG.
 DR InterPro; IPR01007; VMP_C.
 DR Pfam; PF07452; CHRD; 4.
 DR Pfam; PF00093; VMC; 4.
 DR SMART; SM00566; SOG; 3.
 DR SMART; SM00214; VMC; 4.
 DR PROSITE; PS50933; CHRD; 4.
 DR PROSITE; PS501208; VMC_1; 2.
 DR PROSITE; PS50184; VMC_2; 2.
 SQ SEQUENCE 954 AA; 101959 MW; 853117C5D1739E63 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 954;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LLSGLLGG 11
 |||||
 Db 13 LLSGLLGG 20

```

RESULT 47
AA089285 PRELIMINARY; PRT; 954 AA.
ID AA089285;
AC AA089285;
DT 02-MAR-2004 (TEMBREL. 27, Created)
DT 02-MAR-2004 (TEMBREL. 27, Last sequence update)
DT 02-MAR-2004 (TEMBREL. 27, Last annotation update)
DE Chordin.
GN UNQ217.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP PubMed=12975309;
RA Clark H.P., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark W., Robble E., Sanchez C., Schoenfeld J.,
Sehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P.;
RA "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL: AY58926; AA089285.1; -.
SQ SEQUENCE 954 AA; 101959 MW; 853317CSD1739E63 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 954;
Best Local Similarity 100.0%; Pred.No.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LGLGLLGG 11
Db 13 LGLGLLGG 20

RESULT 48
CHRD_HUMAN STANDARD; PRT; 955 AA.
ID CHRD_HUMAN;
AC Q9H2X0; O95254; Q9H2D3; Q9H2W8; Q9H2W9; Q9P0Z2; Q9P0Z3; Q9P0Z4;
AC Q9P0Z5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chordin precursor.
GN Name=CHRD;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RP MEDLINE=21366001; PubMed=11472837;
RA Millet C., Lemaire P., Orsetti B., Guglielmi P., Francois V.;
RT "The human chordin gene encodes several differentially expressed
RT spliced variants with distinct BMP opposing activities.";
RL Mech. Dev. 106:85-96(2001).

[2]
SEQUENCE OF 115-955 FROM N.A. (ISOFORM 5).
RP MEDLINE=9900848; PubMed=782094;
RA Pappano W.N., Scott I.C., Clark T.G., Eddy R.L., Shows T.B.,
RA Greenpan D.S.;
RT "Coding sequence and expression patterns of mouse chordin and mapping
RT of the cognate mouse chrd and human CHRD genes.";
RL Genomics 52:236-239(1998).

[3]

```

```

RP SEQUENCE OF 51-125; 705-762; 784-850 AND 872-932 FROM N.A.
RX MEDLINE=20115435; PubMed=10648240;
RA Iarrain J., Bachiller D., Lu B., Agius E., Piccolo S.,
RA de Robertis E.M.;
RT "BMP-binding modules in chordin: a model for signalling regulation in
RT the extracellular space.";
RL Development 127:821-830(2000).

[4]
RP SPICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.B.;
RT "An unappreciated role for RNA surveillance.";
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
CC -1- FUNCTION: Dorsalizing factor. Key developmental protein that
CC dorsalizes early vertebrate embryonic tissues by binding to
CC and sequestering them in latent complexes (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC isoforms;
CC Name=1;
CC IsoId=Q9H2X0-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9H2X0-2; Sequence=VSP_001069, VSP_001070;
CC Name=3;
CC IsoId=Q9H2X0-3; Sequence=VSP_001071, VSP_001072;
CC Note=May be produced at very low levels due to a premature stop
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC Name=4;
CC IsoId=Q9H2X0-4; Sequence=VSP_001073, VSP_001074;
CC Note=May be produced at very low levels due to a premature stop
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC Name=5;
CC IsoId=Q9H2X0-5; Sequence=VSP_001075;
CC -1- TISSUE SPECIFICITY: Expressed at the highest level in liver.
CC -1- SIMILARITY: Belongs to the chordin family.
CC -1- SIMILARITY: Contains 4 CHRD domains.
CC -1- SIMILARITY: Contains 4 WWC domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF209928; AAC35767.1; -.
CC EMBL: AF209929; AAC35768.1; -.
CC EMBL: AF209930; AAC35769.1; -.
CC EMBL: AF076612; AAC69835.1; -.
CC EMBL: AF283325; AAC35784.1; -.
CC EMBL: AF136632; AAF70236.1; -.
CC EMBL: AF136633; AAF70237.1; -.
CC EMBL: AF136634; AAF70238.1; -.
CC EMBL: AF136635; AAF70239.1; -.
CC GeneW; HGNC:1949; CHRD.
CC MIM; 603475; -.
CC GO; GO:0001501; P:skeletal development; TAS.
CC InterPro; IPR010895; CHRD.
CC InterPro; IPR001007; WWC_C.
CC Pfam; PF07452; CHRD; 4.
CC Pfam; PF00093; WWC; 4.
CC PROSITE; PS50933; CHRD; 4.
CC PROSITE; PS01208; WWC_1; 2.
CC PROSITE; PS0184; WWC_2; 2.
CC KW Alternative splicing; Developmental protein; Glycoprotein; Repeat;
CC Signal.
CC FT 1 26 Potential.
CC FT 27 955 Chordin.
CC FT 49 126 WWC 1.
CC DOMAIN

```

```

FT DOMAIN 168 277 CHRD 1.
FT DOMAIN 279 402 CHRD 2.
FT DOMAIN 403 524 CHRD 3.
FT DOMAIN 530 650 CHRD 4.
FT DOMAIN 703 763 VMFC 2.
FT DOMAIN 784 850 VMFC 3.
FT DOMAIN 872 932 VMFC 4.
FT CARBOHYD 217 217 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 351 351 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 365 365 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 434 434 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 85 86 PO -> GP (in isoform 2).
FT VARSPLIC 87 955 Missing (in isoform 2).
FT VARSPLIC 85 94 Missing (in isoform 3).
FT VARSPLIC 95 955 Missing (in isoform 3).
FT VARSPLIC 328 350 Missing (in isoform 4).
FT VARSPLIC 351 955 Missing (in isoform 4).
FT VARSPLIC 441 480 Missing (in isoform 5).
FT CONFLICT 115 118 ROLP -> QVAA (in Ref. 2).
FT CONFLICT 189 189 V -> A (in Ref. 2).
FT CONFLICT 216 216 S -> P (in Ref. 2).
FT CONFLICT 674 674 T -> P (in Ref. 2).
SQ SEQUENCE 955 AA; 102013 MW; 12AC030CEACFP3ED CRC64;

```

Query Match Best Local Similarity 2.5%; Score 8; DB 1; Length 955; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGGLLGL 11
Db 13 LIGGLLGL 20

```

RESULT 49
ID 086G86 PRELIMINARY; PRT; 975 AA.
AC 086G86;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Integrin alpha 3.
OS Pseudoplasia includens (Soybean looper).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Noctuoidea;
OC Noctuidae; Plusiinae; Pseudoplasia.
OC NCBI_TaxID=76492;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2285736; PubMed=12974949;
RA Lavine M.D., Strand M.R.;
RT "Haemocytes from Pseudoplasia includens express multiple alpha and
RT beta integrin subunits."
RL Insect Mol. Biol. 12:441-452(2003).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; AY337587; AAC85805.1; -.
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR000413; Integrin_alpha.
DR Pfam; PF01839; FG-GAP; 2.
DR PRINTS; PRO1185; INTEGRIN.
DR SMART; SM00191; Int_alpha; 6.
DR PROSITE; PS00242; INTEGRIN ALPHA; UNKNOWN_1.
KM Cell adhesion; Integrin; Transmembrane.

```

```

SQ SEQUENCE 975 AA; 108890 MW; 174CB0F89F311AD8 CRC64;
Query Match Best Local Similarity 2.5%; Score 8; DB 2; Length 975;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 LIGGLLGL 11
Db 907 LIGGLLGL 914

```

RESULT 50

```

ID CPBX_CAVPO STANDARD; PRT; 20 AA.
AC P34033;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cytochrome P45011B (EC 1.14.14.1) (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OC NCBI_TaxID=10141;
RN [1]
RP SEQUENCE AND CHARACTERIZATION.
RC STRAIN=Hartley; TISSUE=Liver.
RX MEDLINE=91054472; PubMed=2173574;
RA Narimatsu S., Aizawa Y., Matsumura T., Watanabe K., Yamamoto I.,
RA Yoshimura H.;
RT Purification of a cytochrome P450 isozyme belonging to a subfamily of
RT P450 11B from liver microsomes of guinea pigs."
RL Biochem. Biophys. Res. Commun. 172:607-613(1990).
CC -1- FUNCTION: Cytochromes P450 are a group of heme-thiolate
CC monooxygenases. In liver microsomes, this enzyme is involved in an
CC NADPH-dependent electron transport pathway. This isozyme is active
CC upon P-nitroanisole, aniline, D-benzphetamine, delta(9)-
CC tetrahydrocannabinol (THC) and strychnine.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR InterPro; IPR001128; Cytochrome_P450.
DR PROSITE; PS00086; CYTOCHROME_P450; PARTIAL.
KM Direct protein sequencing; Electron transport; Endoplasmic reticulum;
KM Heme; Membrane; Microsome; Monooxygenase; Oxidoreductase.
FT NON TER 20
SQ SEQUENCE 20 AA; 2259 MW; 78DC81280C970A55 CRC64;

```

Query Match Best Local Similarity 2.2%; Score 7; DB 1; Length 20; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGGLLGL 10
Db 12 LIGGLLGL 18

```

RESULT 51
ID 09QV45 PRELIMINARY; PRT; 31 AA.
AC 09QV45;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Cytochrome P450 GP-1, P450GP-1 PB (Fragment).
OS Cavia (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae.
OC NCBI_TaxID=10140;
RN [1]
RP SEQUENCE.
RX MEDLINE=93073973; PubMed=1444463;
RA Yamada H., Kaneko H., Takeuchi K., Oguri K., Yoshimura H.;

```

RT "Tissue-specific expression, induction, and inhibition through
RT metabolic intermediate-complex formation of guinea pig cytochrome P450
RT belonging to the CYP2B subfamily."
RL Arch. Biochem. Biophys. 239:248-254(1992).
SQ SEQUENCE 31 AA; 3396 MW; F05B04E2557459AC CRC64;

Query Match 2.2%; Score 7; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
Db 12 LIGLILL 18

RESULT 52

Q9QVU4 PRELIMINARY; PRT; 33 AA.

AC Q9QVU4; 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome P450GP-1 (Fragment).
OS Cavia (guinea pigs).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae.
OX NCBI_TaxID=10140;

RN [1]
RP SEQUENCE
RX MEDLINE=91378369; PubMed=1897986;
RA Oguri K., Kaneko H., Tanimoto Y., Yamada H., Yoshimura H.;
RT "A constitutive form of guinea pig liver cytochrome P450 closely
RT related to phenobarbital inducible P450b(e)."
RL Arch. Biochem. Biophys. 287:105-111(1991).
DR PIR; S15135; A36154.
FT NON_TER 33
SQ SEQUENCE 33 AA; 3550 MW; 1202B05B04E25574 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
Db 12 LIGLILL 18

RESULT 53

Q9QVY1 PRELIMINARY; PRT; 41 AA.

AC Q9QVY1; 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome P4502B (Fragment).
OS Cavia (guinea pigs).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae.
OX NCBI_TaxID=10140;

RN [1]
RP SEQUENCE
RX MEDLINE=96118203; PubMed=8553686;
RA Chung W.G., Miranda C.L., Bulter D.R.;
RT "A cytochrome P4502B form is the major bioactivation enzyme for the
RT pyrolicidine alkaloid senecionine in guinea pig."
RL Xenobiotica 25:929-939(1995).
SQ SEQUENCE 41 AA; 4409 MW; C414BCAF317671C0 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10

Db 12 LIGLILL 18

RESULT 54

Q70BW1 PRELIMINARY; PRT; 42 AA.

AC Q70BW1; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fatty acid hydroxylase (Fragment).
GN Name=CYP4A24;
OS Sus acrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

RN [1]
RP SEQUENCE FROM N.A.
RA Lundell K.;
RT "The porcine taurochenodeoxycholic acid galpha-hydroxylase (CYP 4A21)
RT gene: evolution by gene duplication and gene conversion."
RL Biochem. J. 378:1053-1058(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Lundell K.L.;
RT Submitted (Oct-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ586860; CAB52547.1; -.
FT NON_TER 42
SQ SEQUENCE 42 AA; 4513 MW; 1988CE9A17371985 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
Db 18 LIGLILL 24

RESULT 55

Q70BW2 PRELIMINARY; PRT; 42 AA.

AC Q70BW2; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Taurochenodeoxycholic 6 alpha-hydroxylase (Fragment).
GN Name=CYP4A21;
OS Sus acrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

RN [1]
RP SEQUENCE FROM N.A.
RA Lundell K.L.;
RT "The porcine taurochenodeoxycholic acid galpha-hydroxylase (CYP 4A21)
RT gene: evolution by gene duplication and gene conversion."
RL Biochem. J. 378:1053-1058(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Lundell K.L.;
RT Submitted (Oct-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ586859; CAB52546.1; -.

FT NON_TER 42
SQ SEQUENCE 42 AA; 4560 MW; 05642E7407371985 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10

Db 18 LIGULL 24

RESULT 56
ID CAE52546 PRELIMINARY; PRT; 42 AA.
AC CAE52546;
DT 03-MAR-2004 (TrEMBLrel. 27, Created)
DT 03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 03-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Taurochenodeoxycholic 6 alpha-hydroxylase (Fragment).
GN CYP4A21.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lundell K.;
RT "The porcine taurochenodeoxycholic acid 6alpha-hydroxylase (CYP 4A21) gene: evolution by gene duplication and gene conversion.";
RL Biochem. J. 378:1053-1058(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Lundell K.L.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ586859; CAE52546.1; -.
FT NON TER 42
SQ SEQUENCE 42 AA; 4560 MW; 05642E7407371985 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4 LIGULL 10
Db 18 LIGULL 24

RESULT 57
ID CAE52547 PRELIMINARY; PRT; 42 AA.
AC CAE52547;
DT 03-MAR-2004 (TrEMBLrel. 27, Created)
DT 03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 03-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Fatty acid hydroxylase (Fragment).
GN CYP4A24.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lundell K.;
RT "The porcine taurochenodeoxycholic acid 6alpha-hydroxylase (CYP 4A21) gene: evolution by gene duplication and gene conversion.";
RL Biochem. J. 378:1053-1058(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Lundell K.L.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ586860; CAE52547.1; -.
FT NON TER 42
SQ SEQUENCE 42 AA; 4513 MW; 1988CE9A17371985 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4 LIGULL 10
Db 18 LIGULL 24

RESULT 58
ID Q9UN20 PRELIMINARY; PRT; 44 AA.
AC Q9UN20;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fc gamma receptor III-A (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Song Y.W., Hong K.M., Shin C.H.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162790; AAD48438.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
KW Receptor.
FT NON TER 1
SQ SEQUENCE 44 AA; 5003 MW; 0A7B2538B46395DF CRC64;

Query Match 2.2%; Score 7; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 205 DSGSYFC 211
Db 18 DSGSYFC 24

RESULT 59
ID Q8U2N4 PRELIMINARY; PRT; 66 AA.
AC Q8U2N4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein PF0799.
GN OrderedLocustNames=PF0799.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RX MEDLINE=21079003; PubMed=11210495;
RA Robb F.T., Maeder D.L., Brown J.R., DiRuggiero J., Stump M.D., Yeh R.K., Weiss R.B., Dunn D.M.;
RT "Genomic sequence of hyperthermophile, Pyrococcus furiosus: implications for physiology and enzymology.";
RL Meth. Enzymol. 330:134-157(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010196; AAL80923.1; -.
DR HSSP; P11759; IMFZ.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR002005; NAD BS.
DR InterPro; IPR001732; UDPG_MGDP_dh.
DR Pfam; PF03721; UDPG_MGDP_dh_N; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 66 AA; 7127 MW; B5742284CF9E7FDE CRC64;

Query Match 2.2%; Score 7; DB 2; Length 66;

Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 AVTADSG 207
|||||
Db 21 AVTADSG 27

RESULT 60

07ZH08 PRELIMINARY; PRT; 70 AA.
AC 07ZH08
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=TTIC1687;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=262724;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15064768;
RA Henne A., Brueggemann H., Raasch C., Wierzer A., Hartsch T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacobi C., Starkuviene V., Schlenceck S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.,
RT "The genome sequence of the extreme thermophile Thermus
thermophilus.";
RL Nat. Biotechnol. 22:547-553(2004).
DR EMBL; AB017306; AAS82029.1; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 70 AA; 7957 MW; 33C85B32786D2144 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 16 LIGLILL 22

RESULT 61

AAS82029 PRELIMINARY; PRT; 70 AA.
AC AAS82029
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
GN TTC1687.
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=262724;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15064768;
RA Henne A., Brueggemann H., Raasch C., Wierzer A., Hartsch T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacobi C., Starkuviene V., Schlenceck S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.,
RT "The genome sequence of the extreme thermophile Thermus
thermophilus.";
RL Nat. Biotechnol. 22:547-553(2004).
DR EMBL; AB017306; AAS82029.1; -;
KW Hypothetical protein.
SQ SEQUENCE 70 AA; 7957 MW; 33C85B32786D2144 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 97;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 16 LIGLILL 22

RESULT 62

08TE42 PRELIMINARY; PRT; 77 AA.
AC 08TE42
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Truncated steroid 21-hydroxylase (EC 1.14.99.10).
GN Name=CYP21,
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21601921; PubMed=11739456;
RA Lau I.F., Soardi F.C., Lemos-Martini S.H., Guerra-Jr G., Baptista M.T.,
RA de Mello M.P.;
RT "H28-C insertion in the CYP21 gene: a novel frameshift mutation in a
RT deficiency.";
RL J. Clin. Endocrinol. Metab. 86:5877-5880(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Lau I.F.;
RT "Novel Mutations in CYP21 Gene."
RL Thesis (2000), Department of Institute of Biological Sciences,
RL Campinas State University, Campinas, SP, Brazil.
RN [3]
RP SEQUENCE FROM N.A.
RX de Mello M.P.;
RA Submitted (FEB-2002) to the EMBL/Genbank/DDSI databases.
DR EMBL; A4331212; CND24050.1; -;
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004509; F:steroid 21-monooxygenase activity; IEA.
KW Oxidoreductase.
SQ SEQUENCE 77 AA; 8364 MW; ABAFFP3692422B9C CRC64;

Query Match 2.2%; Score 7; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 3 LIGLILL 9

RESULT 63

07UJ23 PRELIMINARY; PRT; 85 AA.
AC 07UJ23
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=RB3559;
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heltmann K., Rabus R.,

RA Schleener H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 RL strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
 DR EMBL; BX294139; CAD73261.1; -.
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 85 AA; 9616 MW; 797D3DA4F0299FE9 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 85;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 LKTKTE 242
 |||||
 Db 18 LKTKTE 24

RESULT 64

08FEV3 PRELIMINARY; PRT; 88 AA.
 AC 08FEV3;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE GnaB protein.
 GN OrderedLocustNames=c3176;
 OS Escherichia coli O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 CX NCBI_TaxID=217992;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=06:HI / CFT073 / ATCC 700928;
 RX MEDLINE=22388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Raeko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
 DR EMBL; AE016765; AA081628.1; -.
 KM Complete proteome.

SQ SEQUENCE 88 AA; 10413 MW; 238B8BDC1D4501BF CRC64;

Query Match 2.2%; Score 7; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 237 LKTKTEA 243
 |||||
 Db 37 LKTKTEA 43

RESULT 65

08K4N9 PRELIMINARY; PRT; 92 AA.
 ID 08K4N9;
 AC 08K4N9;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Initiate factor 3.2.
 GN Name=Oosp1; Synonym=IF3 2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=2222142; PubMed=12237121;
 RA Mano H., Nakatani S., Aoyagi R., Iehai R., Iwai Y., Shinoda N.,
 RA Jincho Y., Hura H., Hirose M., Mochizuki C., Yuri M., Im R.-H.,
 RA Funada-Wada U., Wada M.;

RT "IF3, a novel cell-differentiation factor, highly expressed in the
 RT murine liver and ovary.";
 RL Biochem. Biophys. Res. Commun. 297:323-328 (2002).
 DR EMBL; AB086437; BAC11848.1; -.
 DR MGI; MGI:2149290; Oosp1.
 SQ SEQUENCE 92 AA; 10597 MW; FC458C6E10005FDA CRC64;

Query Match 2.2%; Score 7; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LLGLLL 10
 |||||
 Db 7 LLGLLL 13

RESULT 66

083JUS PRELIMINARY; PRT; 95 AA.
 ID 083JUS;
 AC 083JUS;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=EP1833;
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 CX NCBI_TaxID=1351;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=V583 / ATCC 700802;
 RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613.
 RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.R., Seshadri R.,
 RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
 RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
 RA Dagherty S.C., Debey R.T., Durkin S.A., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
 RA Kouri H.M., Uetreback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
 RA Frazer C.M.;
 RT "Role of mobile DNA in the evolution of vancomycin-resistant
 RT Enterococcus faecalis.";
 RL Science 299:2071-2074 (2003).
 DR EMBL; AE016952; AAC01598.1; -.
 DR TIGR; BP1833; -.

KM Complete proteome, Hypothetical protein.
 SQ SEQUENCE 95 AA; 10386 MW; 479FF39F72B99EB CRC64;

Query Match 2.2%; Score 7; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LLGLLL 10
 |||||
 Db 36 LLGLLL 42

RESULT 67

016755 PRELIMINARY; PRT; 97 AA.
 ID 016755;
 AC 016755;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Steroid 21-monooxygenase (BC 1.14.99.10) (Fragment).
 GN Name=CYP21A/CYP21B fusion gene;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral blood;
 RX MEDLINE=92297162; PubMed=1605859;

RA Helmborg A., Tabarelli M., Fuchs M.A., Keller E., Dobler G.,
 RA Schlegel I., Knorr D., Albert E., Kofler R.;
 RT "Identification of molecular defects causing congenital adrenal
 RT hyperplasia by cloning and differential hybridization of polymerase
 RT chain reaction-amplified 21-hydroxylase (CYP21) genes.";
 RL DNA Cell Biol. 11:359-368(1992).
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 DR EMBL; X58908; CAA41711.1; -.
 DR PIR; S26485; S26485.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.
 DR GO; GO:0004509; F:steroid 21-monooxygenase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR InterPro; IPR002401; EP4501.
 DR Pfam; PF00067; P450; 1.
 DR PRINTS; PR00463; EP4501.
 KM Heme; Monooxygenase; Oxidoreductase.
 FT NON_TER
 SQ SEQUENCE 97 AA; 11069 MW; 84A118F6680C6737 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
 |||||
 Db 3 LIGLILL 9

RESULT 68
 ID Q8G66 PRELIMINARY; PRT; 97 AA.
 AC Q8G66;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative v-SNARE ALVT1b (At1g26670).
 GN Name=At1g26670/T24P13.20;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RP SEQUENCE FROM N.A.
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinozaki K.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Huan V.W.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN EMBL; AK18409; BAC43018.1; -.
 DR EMBL; BT004676; AAC42922.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006861; P:intracellular protein transport; IEA.
 DR InterPro; IPR007705; V-SNARE.
 DR Pfam; PF05008; V-SNARE; 1.
 SQ SEQUENCE 97 AA; 11149 MW; 41AAA73C1DCC730 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 AIIILIS 292
 |||||

Db 86 AIIILIS 92

RESULT 69
 ID Q950L7 PRELIMINARY; PRT; 98 AA.
 AC Q950L7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE NADH dehydrogenase subunit 4L (EC 1.6.5.3).
 GN Name=nd4L;
 OS Rhizophydium sp. 136.
 OG Mitochondrion.
 OC Eukaryota; Fungi; Chytridiomycota; Chytridiales; Chytridiaceae;
 OC Rhizophydium.
 OX NCBI_TaxID=60187;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=136;
 RX MEDLINE=21651207; PubMed=11861890;
 RA Forget L., Uetlinova J., Wang Z., Huse V.A.R., Lang B.F.;
 RT "Hydrophidium curvatum: a linear mitochondrial genome, tRNA editing,
 RT and an evolutionary link to lower fungi.";
 RL Mol. Biol. Evol. 19:310-319(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=136;
 RA Lang B.F.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF040306; AAK84291.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0006137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
 DR GO; GO:0014391; F:oxidoreductase activity; IEA.
 DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. .; IEA.
 DR InterPro; IPR001133; Oxidored_4L.
 DR InterPro; IPR003214; Oxidored_4L.
 DR Pfam; PF00420; Oxidored_Q2; 1.
 DR Prodom; PD000359; Oxidred4L; 1.
 KM Mitochondrion; Oxidoreductase.
 SQ SEQUENCE 98 AA; 10822 MW; BF4784FP2D7BC5FC CRC64;

Query Match 2.2%; Score 7; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 IILILSL 293
 |||||
 Db 35 IILILSL 41

RESULT 70
 ID Q8G55 PRELIMINARY; PRT; 100 AA.
 AC Q8G55;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Chemokine ah189 (Macrophage inflammatory protein 3alpha).
 GN Name=MP-3alpha;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21655115; PubMed=11797102;
 RA Hughes S., Haynes A., O'Regan M., Burnstead N.;
 RT "Identification, mapping, and phylogenetic analysis of three novel
 RT chicken CC chemokines.";
 RL Immunogenetics 53:674-683(2001).
 RN [2]


```

RP SEQUENCE FROM N.A.
RA Hughes S.M., Bunnstead N.,
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn H-B15; TISSUE=Spleen;
RA Sayed A., Horuchi H., Furusawa S., Matsuda H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn H-B15; TISSUE=Spleen;
RA Sayed A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037861; AK84434.1; -.
DR EMBL; AB101005; BACS5967.1; -.
DR HSSP; P78556; IM8A.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:immune response; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00139; SCY; 1.
SQ SEQUENCE 100 AA; 1149 MW; BE4F16809FCB8778 CRC64;

Query Match      2.2%; Score 7; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LGULLL 10
Db 14 LGULLL 20

RESULT 71
ID YGV4 YEAST STANDARD; PRT; 101 AA.
AC P53089;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical 11.4 kDa protein in FOX1-KEX1 intergenic region.
GN OrderedLocustNames=YGL204C;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Baktaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Bjournson A.J., McReynolds A.D.K., Wright L.F.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z72726; CA96916.1; -.
DR PIR; S64322; S64322.
DR GerMOnline; 141352; -.
DR SGD; S0003172; YGL204C.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 20 40 Potential.
FT TRANSMEM 59 79 Potential.
SQ SEQUENCE 101 AA; 11351 MW; 695B5D009E211566 CRC64;

Query Match      2.2%; Score 7; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LGULLL 11
Db 5 LGULLL 11

```

```

Db 33 LGULLL 39

RESULT 72
ID AAS56831 PRELIMINARY; PRT; 101 AA.
AC AAS56831;
DT 25-MAR-2004 (TREMBlrel. 27, Created)
DT 25-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 25-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE YGL204C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Baktaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Marsischky G., Rolfs A., Richardson A., Kane M., Bagui M., Taycher E.,
RA Hu Y., Vanberg F., Weger J., Kramer J., Moreira D., Kelley F.,
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
RA Gonzalez L., Vasconcelos A.T., Simpson A., Koldner R., Harlow E.,
RA Labaer J.;
RT "Creation of the YPLex clone resource: cloning of Saccharomyces
RT cerevisiae ORFs in the Gateway recombinational cloning system.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY58505; AAS56831.1; -.
SQ SEQUENCE 101 AA; 11351 MW; 695B5D009E211566 CRC64;

Query Match      2.2%; Score 7; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LGULLL 11
Db 33 LGULLL 39

RESULT 73
ID PLF4 RAT STANDARD; PRT; 105 AA.
AC P06765;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Platelet factor 4 precursor (PF-4) (CXCL4).
GN Name=PF4; Synonyms=Scyb4;
OS Rattus norvegicus (Rat).
OC Baktaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87144263; PubMed=3821732;
RA Dot T., Greenberg S.M., Rosenberg R.D.;
RT "Structure of the rat platelet factor 4 gene: a marker for
RT megakaryocyte differentiation.";
RL Mol. Cell. Biol. 7:898-904(1987).
RN [2]
RP O-GLYCOSYLATION.
RX MEDLINE=94307262; PubMed=8031893;
RA Ravanat C., Gachet C., Herbert J.-M., Schuhler S., Guillemot J.-C.,
RA Usabigaga F., Picard C., Ferrara P., Freund M., Cazenave J.-P.;
RT "Rat platelets contain glycosylated and non-glycosylated forms of
RT platelet factor 4. Identification and characterization by mass
RT spectrometry.";
RL Eur. J. Biochem. 223:203-210(1994).
CC -1- FUNCTION: Platelet factor 4, noncovalently bound to a proteoglycan
CC molecule, is released during platelet aggregation. PF4 neutralizes
CC the anticoagulant effect of heparin because it binds more strongly
CC to heparin than to the chondroitin-4-sulfate chains of the carrier
CC molecule. Chemotactic for neutrophils and monocytes.
CC -1- SUBUNIT: Homotetramer.

```

```

CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-linked glycan consists of gal-galNAc disaccharide which is
CC modified with sialic acid residues (microheterogeneity).
CC -1- SIMILARITY: Belongs to the interleukin alpha (chemokine Cxcl)
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M15254; AAA41832.1; -.
CC PIR: A26774; A26774.
CC HSSP: P02776; IRHP.
CC DR GO: GO:0005576; C:extracellular; ISS.
CC DR GO: GO:0008009; F:chemokine activity; ISS.
CC DR GO: GO:0008201; F:heparin binding; ISS.
CC DR GO: GO:0019721; P:cytokine and chemokine mediated signaling p. .; ISS.
CC DR GO: GO:0030595; P:immune cell chemotaxis; ISS.
CC DR GO: GO:0016525; P:negative regulation of angiogenesis; ISS.
CC DR GO: GO:0045653; P:negative regulation of megakaryocyte differ. .; ISS.
CC DR GO: GO:0030168; P:platelet activation; ISS.
CC DR InterPro: IPR002473; C-X-C/Interlkn_8.
CC DR InterPro: IPR001811; Chemokine_Ila.
CC DR InterPro: IPR001089; CXCL_Chemokine_Ila.
CC DR Pfam: PF00048; IL8; 1.
CC DR PRINTS: PR00436; INTERLEUKIN8.
CC DR SMART: SM00437; SMALLCYTCKCX.
CC DR SMART: SM00139; SCY; 1.
CC DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
CC DR Chemotaxis; Cytokine; Glycoprotein; Heparin-binding; Platelet; Signal.
CC KM SIGNAL 1 29
CC FT CHAIN 30 105 Platelet factor 4.
CC FT DISULFID 44 71 By similarity.
CC FT DISULFID 46 87 By similarity.
CC FT CARBOHYD 31 31 O-linked (GalNAc...); partial.
CC SQ SEQUENCE 105 AA; 11286 MW; D9CCAD26A284496 CRC64;

Query Match 2.2%; Score 7; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
DB 18 LGGLLL 24

RESULT 74
Q70HT8 PRELIMINARY; PRT; 105 AA.
AC Q70HT8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE V1ha protein (Fragment).
GN Name=V1ha;
OS Mycoplasma synoviae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2109;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K4;
RA Hammond P.P., Hazel K., Bradbury J.M., Morrow C.J.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B133-99-5;
RA Hammond P.P., Bradbury J.M., Ramirez A.S., Morrow C.J.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ580984; CAE45731.1; -.

```

```

DR EMBL; AJ580983; CAE45730.1; -.
DR InterPro: IPR002988; GA.
DR Pfam: PR01468; GA; 1.
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 10464 MW; 4BC03E36A1421D67 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 LKTKTEA 243
DB 86 LKTKTEA 92

RESULT 75
CAE45730 PRELIMINARY; PRT; 105 AA.
AC CAE45730;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE V1ha protein (Fragment).
GN V1ha.
OS Mycoplasma synoviae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2109;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B133-99-5;
RA Hammond P.P., Bradbury J.M., Ramirez A.S., Morrow C.J.;
RT "Combined detection and identification of Mycoplasma synoviae strains
RT by amplification of a conserved part of the V1ha gene."
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ580983; CAE45730.1; -.
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 10464 MW; 4BC03E36A1421D67 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 LKTKTEA 243
DB 86 LKTKTEA 92

Search completed: January 4, 2005, 07:02:43
Job time : 122 secs

```


ALIGNMENTS

RESULT 1

154768
epididymis-specific four-disulfide core protein CE4 - dog
C/Species: Canis lupus familiaris (dog)
C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C/Accession: I54768
R/Elberbrock, K.; Pera, I.; Hartung, S.; Ivell, R.
Int. J. Androl. 17, 314-323, 1994
A/Title: Gene expression in the dog epididymis: a model for human epididymal function.
A/Reference number: I54768; MUID:95263175; PMID:7744511
A/Accession: I54768
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-124 <BL>
A/Cross-references: UNIPROT:Q28894; GB:S77395; NID:g945180; PIDN:AA834264.1; PID:g945181
C/Superfamily: antileukoprotease; antileukoprotease repeat homology
F/76-123/Domain: antileukoprotease repeat homology <ALP>

Query Match

Best Local Similarity 2.5%; Score 8; DB 2; Length 124;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILIG 11
|||||
Db 14 LIGLILIG 21

RESULT 2

H83359
hypothetical protein PA2284 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: H83359
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Badian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam, N.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: H83359
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-223 <STO>
A/Cross-references: UNIPROT:Q911J1; GB:AE004654; GB:AE004091; NID:g9948311; PIDN:AA60567
C/Genetic: PA2284
A/Gene: PA2284

Query Match

Best Local Similarity 2.5%; Score 8; DB 2; Length 223;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILIG 11
|||||
Db 47 LIGLILIG 54

RESULT 3

A69256
hypothetical protein AF0049 - Archaeoglobus fulgidus
C/Species: Archaeoglobus fulgidus
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: A69256
R/Klem, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Godek, A.; Zhou, L.; Overbeek, R.; Goeyne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A/Authors: Uiterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon

A/Reference number: A69250; MUID:98049343; PMID:9389475

A/Accession: A69256
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-412 <MLE>
A/Cross-references: UNIPROT:Q30187; GB:AE001103; GB:AE000782; NID:g2689426; PIDN:AA89117

Query Match

Best Local Similarity 2.5%; Score 8; DB 2; Length 412;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 YIGETISAG 277
|||||
Db 142 YIGETISAG 149

RESULT 4

JC5889
OS-9 protein precursor - human
N/Contains: OS-9 protein, splice form 1; OS-9 protein, splice form 2; OS-9 protein, splice form 3
C/Species: Homo sapiens (man)
C/Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 09-Jul-2004
C/Accession: JC5889; J0106; J0107; J0108
R/Kimura, Y.; Nakazawa, M.; Tsuchiya, N.; Asakawa, S.; Shimizu, N.; Yamada, M.
J. Biochem. 122, 1190-1195, 1997
A/Title: Genomic organization of the OS-9 gene amplified in human sarcomas.
A/Reference number: JC5889; MUID:98158329; PMID:9498564
A/Accession: JC5889
A/Molecule type: DNA
A/Residues: 1-667 <KIM1>
A/Cross-references: UNIPROT:Q13438; DDBJ:AB002806; NID:g2780782; PIDN:BAA24363.1; PID:dl
A/Experimental source: sarcomas

A/Note: neither the complete nucleic acid sequence nor the complete translation are shown
R/Kimura, Y.; Nakazawa, M.; Yamada, M.
J. Biochem. 123, 876-882, 1998
A/Title: Cloning and characterization of three isoforms of OS-9 cDNA and expression of the
A/Reference number: J0108; MUID:98230694; PMID:9562620
A/Accession: J0106
A/Molecule type: mRNA
A/Residues: 1-667 <KIM2>
A/Cross-references: DDBJ:AB002806; NID:g2780782; PIDN:BAA24363.1; PID:dl025275; PID:g278

A/Accession: J0107
A/Molecule type: mRNA
A/Residues: 1-534,590-667 <KIM3>
A/Cross-references: DDBJ:AB002806
A/Accession: J0108
A/Molecule type: mRNA
A/Residues: 1-455,471-534,590-667 <KIM4>
A/Cross-references: DDBJ:AB002806
C/Comment: This protein is involved in amplification and overexpression of various tumor

C/Genetic: OS-9
A/Gene: OS-9
A/Cross-references: GDB:9958646
A/Map position: 12q13-12q15
C/Keywords: alternative splicing; carcinogenesis; glycoprotein
F/1-25/Domain: signal sequence #status predicted <SIG>
F/26-667/Product: OS-9 protein, splice form 1 #status predicted <MAT1>
F/26-534,590-667/Product: OS-9 protein, splice form 2 #status predicted <MAT2>
F/26-455,471-534,590-667/Product: OS-9 protein, splice form 3 #status predicted <MAT3>
F/177/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match

Best Local Similarity 2.5%; Score 8; DB 2; Length 667;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILIG 11
|||||
Db 10 LIGLILIG 17

RESULT 5

A33154
benzphetamine N-demethylase (EC 1.14.14.-) cytochrome P450 2B - guinea pig (fragment)

N/Alternate names: cytochrome P450(GP-1)
 C/Species: *Cavia porcellus* (guinea pig)
 C/Date: 31-Mar-1992 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
 C/Accession: S15135; S28205; A36154
 R/Oguri, K.; Kaneko, H.; Tanimoto, Y.; Yamada, H.; Yoshimura, H.
 Arch. Biochem. Biophys. 287, 105-111, 1991
 A/Title: A constitutive form of guinea pig liver cytochrome P450 closely related to phenanthrene hydroxylase
 A/Reference number: S15135; PMID:91378363; PMID:1897986
 A/Accession: S15135
 A/Molecule type: protein
 A/Residues: 1-33 <ARC>
 A/Cross-references: UNIPROT:Q9GVJ4
 R/Yamada, H.; Kaneko, H.; Takeuchi, K.; Oguri, K.; Yoshimura, H.
 Arch. Biochem. Biophys. 299, 248-254, 1992
 A/Title: Tissue-specific expression, induction, and inhibition through metabolic interme
 A/Reference number: S28205; PMID:9307973; PMID:1444463
 A/Accession: S28205
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-31 <YAM>
 R/Narimatsu, S.; Akutsu, Y.; Matsunaga, T.; Watanabe, K.; Yamamoto, I.; Yoshimura, H.
 Biochem. Biophys. Res. Commun. 172, 607-613, 1990
 A/Title: Purification of a cytochrome P450 isozyme belonging to a subfamily of P450 IIB
 A/Reference number: A36154; PMID:91054472; PMID:2173574
 A/Accession: A36154
 A/Molecule type: protein
 A/Residues: 1-20 <NAR>
 A/Genetics:
 C/Genetics:
 A/Gene: CYP2B
 C/Superfamily: human cytochrome P450 CYP2B6; cytochrome P450 homology
 C/Keywords: electron transfer; endoplasmic reticulum; heme; monooxygenase; oxidoreductase

Query Match 2.2%; Score 7; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LGILLL 10
 Db 12 LGILLL 18

RESULT 6
 S13581
 collagen alpha 1(IX) chain precursor, short splice form - human (fragment)
 C/Species: *Homo sapiens* (man)
 C/Date: 21-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 15-Sep-2003
 C/Accession: S13581; D35980
 R/Muragaki, Y.; Kimura, T.; Nimomiya, Y.; Olsen, B.R.
 Eur. J. Biochem. 192, 703-708, 1990
 A/Title: The complete primary structure of two distinct forms of human alpha-1(IX) colla
 A/Reference number: S13580; PMID:9106164; PMID:2209617
 A/Accession: S13581
 A/Molecule type: mRNA
 A/Residues: 1-43 <MUR>
 A/Cross-references: EMBL:X54413; NID:930087; PIN:CA38277.1; PID:930088
 R/Muragaki, Y.; Nimomiya, I.; Henney, A.; Nimomiya, Y.; Olsen, B.R.
 Proc. Natl. Acad. Sci. U.S.A. 87, 2400-2404, 1990
 A/Title: The alpha 1(IX) collagen gene gives rise to two different transcripts in both m
 A/Reference number: A35980; PMID:90207204; PMID:1690866
 A/Accession: D35980
 A/Molecule type: DNA
 A/Residues: 1-24 <MUR>
 A/Cross-references: EMBL:M32133
 C/Comment: Prolines and lysines at the third position of the tripeptide repeating unit
 C/Genetics:
 A/Gene: GDB:COL9A1
 A/Cross-references: GDB:119794; OMIM:120210
 A/Map position: 6q12-6q14
 A/Intons: 24/3
 C/Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) chain, one alpha 2
 C/Function:
 A/Description: structural component of extracellular fibrous polymer associated with type

A/Note: in corneal epithelium the short splice form is predominantly produced
 C/Keywords: alternative splicing; coll; cornea; extracellular matrix; glycoprote
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/24-43/Product: collagen alpha 1(IX) chain, short splice form (fragment) #status predi
 F/24-25/Domain: non-collagenous NC4 #status predicted <NC4>
 F/26-43/Domain: collagenous COL3 (fragment) #status predicted <COL3>
 F/2/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicte

Query Match 2.2%; Score 7; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LGILLG 11
 Db 11 LGILLG 17

RESULT 7
 S26485
 cytochrome P450 21A/B mutant fusion protein - human
 N/Alternate names: steroid 21-monooxygenase
 C/Species: *Homo sapiens* (man)
 C/Date: 06-Jan-1995 #sequence_revision 17-Aug-1995 #text_change 09-Jul-2004
 C/Accession: S26485; S29672
 R/Helmsberg, A.; Kofler, R.
 submitted to the EMBL Data Library, March 1991
 A/Reference number: S26484
 A/Accession: S26485
 A/Molecule type: DNA
 A/Residues: 1-97 <HEL>
 A/Cross-references: UNIPROT:Q16755; EMBL:X58901
 A/Experimental source: leukocyte clone AGS 8-23
 A/Note: an unequal cross-over mutation of the CYP21P pseudogene and CYP21 gene in a con
 A/Accession: S29672
 A/Molecule type: DNA
 A/Residues: 1-97 <HE2>
 A/Cross-references: EMBL:X58908
 C/Genetics:
 A/Gene: CYP21P/CYP21
 A/Map position: 6p21.3
 A/Intons: 68/1
 C/Keywords: fusion protein

Query Match 2.2%; Score 7; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LGILLL 10
 Db 3 LGILLL 9

RESULT 8
 S64222
 probable membrane protein YGL204C - yeast (*Saccharomyces cerevisiae*)
 N/Alternate names: hypothetical protein G1234
 C/Species: *Saccharomyces cerevisiae*
 C/Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
 C/Accession: S64222
 R/Bourgon, A.J.; McReynolds, A.D. K.; Wright, L.F.
 submitted to the Protein Sequence Database, May 1996
 A/Reference number: S64218
 A/Accession: S64222
 A/Molecule type: DNA
 A/Residues: 1-101 <BBO>
 A/Cross-references: UNIPROT:P53089; EMBL:Z72726; NID:G1322837; PID:G1322838; GSPDB:GN00
 C/Genetics:
 A/Gene: MIP5:YGL204C
 A/Cross-references: SGD:S0003172
 A/Map position: 7L
 C/Superfamily: Saccharomyces probable membrane protein YGL204C
 C/Keywords: transmembrane protein

F;22-38/Domain: transmembrane #status predicted <TM1>
F;60-76/Domain: transmembrane #status predicted <TM2>

Query Match 2.2%; Score 7; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LGILLG 11

|||||

DB 33 LGILLG 39

RESULT 9

A26774

Platelet factor 4 precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004

C/Accession: A26774; S45657

R/Dol, T.; Greenberg, S.M.; Rosenberg, R.D.

Mol. Cell. Biol. 7, 898-904, 1987

A/Title: Structure of the rat platelet factor 4 gene: a marker for megakaryocyte differentiation

A/Reference number: A26774; PMID:87144262; PMID:3821732

A/Accession: A26774

A/Molecule type: DNA, mRNA

A/Residues: 1-105 <DOI>

A/Cross-references: UNIPROT:P06765; GB:M15254; NID:9206090; PIDN:AAA41832.1; PID:9206091

R/Ravanat, C.; Gachet, C.; Herbert, J.M.; Schunhler, S.; Guillemet, J.C.; Uzabiega, F.; F

Eur. J. Biochem. 223, 203-210, 1994

A/Title: Rat platelets contain glycosylated and non-glycosylated forms of platelet factor 4

A/Reference number: S45657; PMID:94307262; PMID:8033893

A/Accession: S45657

A/Molecule type: protein

A/Residues: 30-42 <RAV>

C/Superfamily: beta-thromboglobulin

QY 4 LGILLG 10

|||||

DB 18 LGILLG 24

RESULT 10

A27594

Ig kappa chain precursor V-I region (Na1n-6) - human

C/Species: Homo sapiens (man)

C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jan-2000

C/Accession: A27594

R/Graninger, W.B.; Goldman, P.L.; Morton, C.C.; O'Brien, S.J.; Koremeyer, S.J.

J. Exp. Med. 167, 488-501, 1988

A/Title: The kappa-deleting element. Germ-line and rearranged, duplicated and dispersed forms

A/Reference number: A92779; PMID:8154733; PMID:3126251

A/Accession: A27594

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-116 <GRA>

A/Note: this sequence was translated from an aberrantly rearranged kappa gene from lambda

C/Genetics:

A/Map position: 2

A/Intons: 19/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;1-22/Domain: signal sequence #status predicted <SIG>

F;38-112/Domain: immunoglobulin homology <IMM>

QY 4 LGILLG 10

|||||

DB 9 LGILLG 15

RESULT 11

K1HUI1

Ig kappa chain precursor V-I region (HK101) - human

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 09-Jul-2004

C/Accession: A01881; A21056

R/Bentley, D.L.; Rabbits, T.H.

Nature 288, 730-733, 1980

A/Title: Human immunoglobulin variable region genes - DNA sequences of two V-kappa gene

A/Reference number: A93241; PMID:8109866; PMID:6779204

A/Accession: A01881

A/Molecule type: DNA

A/Residues: 1-117 <BEN1>

A/Cross-references: UNIPROT:P01601; GB:V00558; GB:J00244; GB:J00246; NID:933176; PIDN:C

A/Note: the sequence was determined from the germline gene

R/Bentley, D.L.; Rabbits, T.H.

Cell 32, 181-189, 1983

A/Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplica

A/Reference number: A21056; PMID:83129397; PMID:6402305

A/Accession: A21056

A/Molecule type: DNA

A/Residues: 1-117 <BEN2>

A/Cross-references: GB:K01322; NID:9185993; PIDN:AAA58930.1; PID:9185994

C/Genetics:

A/Map position: 2p12-2p12

A/Intons: 19/1

C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (ka

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1.

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-117/Domain: Ig kappa chain V-I region (HK101) #status predicted <MAT>

F;38-112/Domain: immunoglobulin homology <IMM>

F;45-110/Disulfide bonds: #status predicted

QY 4 LGILLG 10

|||||

DB 9 LGILLG 15

RESULT 12

K1HUI2

Ig kappa chain precursor V-I region (HK102) - human

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 09-Jul-2004

C/Accession: A01882

R/Bentley, D.L.; Rabbits, T.H.

Nature 288, 730-733, 1980

A/Title: Human immunoglobulin variable region genes - DNA sequences of two V-kappa gene

A/Reference number: A93241; PMID:8109866; PMID:6779204

A/Accession: A01882

A/Molecule type: DNA

A/Residues: 1-117 <BEN3>

A/Cross-references: UNIPROT:P01602; GB:J00245; NID:9185981; PIDN:AAA59087.1; PID:9185982

A/Note: the sequence was determined from the germline gene

C/Genetics:

A/Map position: 2p12-2p12

A/Intons: 19/1

C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (ka

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1.

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer

F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-117/Product: Ig kappa chain V-I region (HK102) #status predicted <MAT>
F:38-112/Domain: immunoglobulin homology <IMM>
F:45-110/Distulfide bonds: #status predicted

Query Match 2.2%; Score 7; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
|||
Db 9 LIGLILL 15

RESULT 13

C21056
Ig kappa chain precursor V region (HK137) - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000

C/Accession: C21056
R/Bentley, D.L.; Rabbitts, T.H.

Cell 32, 181-189, 1983

A/Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicated

A/Reference number: A21056; MUID:83129397; PMID:6402305

A/Accession: C21056
A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-117 <BN>

A/Cross-references: GB:J00248; NID:G165991; PIDN:AA59094.1; PID:G165992

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
|||
Db 9 LIGLILL 15

RESULT 14

S41811
Ig kappa chain V region L22 - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000

C/Accession: S41811
R/Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Lamm, R.; Zac

Eur. J. Immunol. 23, 2868-2875, 1993

A/Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequenc

A/Reference number: S41809; MUID:94039386; PMID:8223863

A/Accession: S41811
A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-117 <HDB>

A/Cross-references: EMBL:X72816; NID:G415368; PIDN:CAA51335.1; PID:G4386773

C/Genetics: 19/1
A/Intons: 19/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
|||
Db 9 LIGLILL 15

RESULT 15

S41812

Ig kappa chain V region L24, allelic sequence - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C/Accession: S41812
R/Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Lamm, R.; Za

Eur. J. Immunol. 23, 2868-2875, 1993

A/Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequen

A/Reference number: S41809; MUID:94039386; PMID:8223863

A/Accession: S41812
A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-117 <HDB>

A/Cross-references: EMBL:X72819; NID:G415374; PIDN:CAA51338.1; PID:G415375

C/Genetics: 19/1
A/Intons: 19/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
|||
Db 9 LIGLILL 15

RESULT 16

S24206
Ig kappa chain V region (Vx O12 and Vx O2) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 25-Feb-1994 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

C/Accession: S24206; S24209
R/Pargent, W.; Meindl, A.; Thiebe, R.; Mitzel, S.; Zachau, H.G.

Eur. J. Immunol. 21, 1821-1827, 1991

A/Title: The human immunoglobulin kappa locus. Characterization of the duplicated O reg

A/Reference number: S24205; MUID:91330953; PMID:1907917

A/Accession: S24206
A/Molecule type: DNA

A/Residues: 1-117 <PAR>

A/Cross-references: EMBL:X59315; NID:G33247; PIDN:CAA42002.1; PID:G33248

A/Experimental source: placenta

A/Genetics: G1
A/Accession: S24209

A/Molecule type: DNA
A/Residues: 1-117 <PMW>

A/Cross-references: EMBL:X59312; NID:G33252; PIDN:CAA41999.1; PID:G33253

A/Experimental source: placenta

A/Genetics: G2
C/Genetics: <G1>

A/Accession: S24206
A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-117 <PMW>

A/Cross-references: EMBL:X59312; NID:G33252; PIDN:CAA41999.1; PID:G33253

A/Experimental source: placenta

A/Genetics: G2
C/Genetics: <G1>

A/Accession: S24206
A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-117 <PMW>

A/Cross-references: EMBL:X59312; NID:G33252; PIDN:CAA41999.1; PID:G33253

A/Experimental source: placenta

A/Genetics: G1
A/Accession: S24209

A/Molecule type: DNA
A/Residues: 1-117 <PMW>

A/Cross-references: EMBL:X59312; NID:G33252; PIDN:CAA41999.1; PID:G33253

A/Experimental source: placenta

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
|||
Db 9 LIGLILL 15

RESULT 17

S42264
Ig kappa chain V region (L11) - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C/Accession: S42264
R/Seoet, W.G.; Critchmans, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que
J. Immunol. 147, 4007-4013, 1991
A/Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus inf
A/Reference number: S42263; MUID:92043792; PMID:1940382
A/Accession: S42264
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-117 <SCO>
A/Cross-references: EMBL:M64858; NID:g185952; PIDN:AAA58924.1; PID:g185953
C/Genetics:
A/Intons: 19/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2% Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
 |||||
Db 9 LIGLILL 15

RESULT 18
S11700
Ig kappa chain precursor V-I region - human
C/Species: Homo sapiens (man)
C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S11700
R/Rech, W.; Smola, H.; Pohlentz, H.D.; Straubinger, B.; Gerl, R.; Zachau, H.G.
J. Mol. Biol. 183, 291-299, 1985
A/Title: A large section of the gene locus encoding human immunoglobulin variable region
A/Reference number: S11697; MUID:85264787; PMID:3927006
A/Accession: S11700
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-117 <PEC>
A/Cross-references: EMBL:X17262; NID:g37873; PIDN:CAA5156.1; PID:g296686
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1985
C/Genetics:
A/Intons: 19/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2% Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
 |||||
Db 9 LIGLILL 15

RESULT 19
S10227
Ig kappa chain precursor V region (orphan V108) - human (fragment)
C/Species: Homo sapiens (man)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C/Accession: S10227
R/Huber, C.; Thiebe, R.; Hameister, H.; Smola, H.; Loetscher, E.; Zachau, H.G.
Nucleic Acids Res. 18, 3475-3478, 1990
A/Title: A human immunoglobulin kappa orphan without sequence defects may be the product
A/Reference number: S10227; MUID:90301460; PMID:2114012
A/Accession: S10227
A/Molecule type: DNA
A/Residues: 1-117 <HUB>

A/Cross-references: EMBL:X51887
C/Genetics:
A/Map position: 2q12-q14
A/Intons: 19/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2% Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
 |||||
Db 9 LIGLILL 15

RESULT 20
S41809
Ig kappa chain V region A30 - human
C/Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C/Accession: S41809
R/Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Weindl, A.; Thiebe, R.; Iamm, R.; Za
Bur, J. Immunol. 23, 2868-2875, 1993
A/Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequen
A/Reference number: S41809; MUID:94039386; PMID:8223863
A/Accession: S41809
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-117 <HUB>
A/Cross-references: EMBL:X72808; NID:g415383; PIDN:CAA51328.1; PID:g415384
C/Genetics:
A/Intons: 19/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2% Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
 |||||
Db 9 LIGLILL 15

RESULT 21
B21056
Ig kappa chain precursor V region (HK134) - human (fragment)
C/Species: Homo sapiens (man)
C>Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000
C/Accession: B21056
R/Bentley, D.L.; Rabbits, T.H.
Cell 32, 181-189, 1983
A/Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicat
A/Reference number: A21056; MUID:83129397; PMID:6402305
A/Accession: B21056
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-117 <BEN>
A/Cross-references: GB:K01323; NID:g185995; PIDN:AAA58931.1; PID:g185996
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2% Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
 |||||
Db 9 LIGLILL 15

RESULT 22

S21527
Ig kappa chain precursor V-I region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: S11699; S34076; S34105; S21521; S21527
R:Peck, M.; Smola, H.; Pohlman, H.D.; Straubinger, B.; Gerl, R.; Zachau, H.G.
J. Mol. Biol. 183, 291-299, 1985
A:Title: A large section of the gene locus encoding human immunoglobulin variable region
A:Reference number: S11697; MUID:85264787; PMID:3927006
A:Accession: S11699
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <PBC>
A:Cross-references: EMBL:X17263; NID:937889; PIDN:CAA35167.1; PID:9296687
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989
R:Magner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34076
A:Molecule type: DNA
A:Residues: 30-117 <WA2>
A:Cross-references: EMBL:X66044; NID:933320; PIDN:CAA46843.1; PID:933321; EMBL:X66043; N
A:Experimental source: patient.7
A:Accession: S34105
A:Molecule type: DNA
A:Residues: 30-117 <WAG>
A:Cross-references: EMBL:X66044; NID:933320; PIDN:CAA46843.1; PID:933321
C:Genetics: 19/1
A:Intons: 19/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMW>
Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 LIGLILL 10
Db 9 LIGLILL 15

RESULT 23
S24207
Ig kappa chain V region (Vx 014 and Vx 04) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 25-Feb-1994 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: S24207; S24210
R:Piergent, W.; Meindl, A.; Thiebe, R.; Mitzel, S.; Zachau, H.G.
Eur. J. Immunol. 21, 1821-1827, 1991
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated O regi
A:Reference number: S24205; MUID:9130953; PMID:1907917
A:Accession: S24207
A:Molecule type: DNA
A:Residues: 1-117 <PAR>
A:Cross-references: EMBL:X59316
A:Genetics: G1
A:Accession: S24210
A:Molecule type: DNA
A:Residues: 1-117 <PAM>
A:Cross-references: EMBL:X59313
A:Genetics: G2
C:Genetics: <G1>
A:Gene: Vx 014
A:Map position: 2
A:Intons: 19/1
C:Genetics: <G2>
A:Gene: Vx 04

A:Map position: 2

A:Intons: 19/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMW>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
Db 9 LIGLILL 15

RESULT 24

S41810
Ig kappa chain V region L14 - human
C:Species: Homo sapiens (man)
C>Date: 06-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S41810
R:Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Lamm, R.; Za
Eur. J. Immunol. 23, 2868-2875, 1993
A:Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequen
A:Reference number: S41809; MUID:94039386; PMID:8223863
A:Accession: S41810
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <HUB>
A:Cross-references: EMBL:X63392
C:Genetics: 19/1
A:Intons: 19/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMW>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
Db 9 LIGLILL 15

RESULT 25

S42263
Ig kappa chain V region (08) - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42263
R:Scott, M.G.; Crichton, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Qu
J. Immunol. 147, 4007-4013, 1991
A:Title: Clonal characterization of the human IGG antibody repertoire to Haemophilus in
A:Reference number: S42263; MUID:92043792; PMID:1940382
A:Accession: S42263
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <SCO>
A:Cross-references: EMBL:M64855; NID:9185963; PIDN:AAA58925.1; PID:9185964
A:Genetics: 19/1
A:Intons: 19/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMW>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
Db 9 LIGLILL 15

RESULT 26

S46374
Ig kappa chain V-J region (T33-4) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C/Accession: S46374; S36651
R/Bensimon, C.; Chateigner, P.; Zouali, M.
EMBL J 13, 2951-2962, 1994
A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rearrangement
A/Reference number: S46369; MUID:94333975; PMID:8039491
A/Accession: S46374
A/Molecule type: mRNA
A/Residues: 1-120 <RLE>
A/Cross-references: EMBL:Z27175; NID:g415965; PIDN:CA81699.1; PID:g415966
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/31-105/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 27;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 2 LIGLILL 8

RESULT 27

S40351
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40351
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40351
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-122 <RLE>
A/Cross-references: EMBL:X72461; NID:g441390; PIDN:CA51129.1; PID:g441391
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 28;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 3 LIGLILL 9

RESULT 28

S40314
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40314
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40314
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-122 <RLE>
A/Cross-references: EMBL:X72424
C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin
F/31-105/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 2 LIGLILL 8

RESULT 29

S40370
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40370
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40370
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-122 <RLE>
A/Cross-references: EMBL:X72480; NID:g441428; PIDN:CA51148.1; PID:g441429
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/30-104/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 28;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 1 LIGLILL 7

RESULT 30

S40331
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40331
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40331
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-123 <RLE>
A/Cross-references: EMBL:X72441; NID:g441350; PIDN:CA51109.1; PID:g441351
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 28;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 3 LIGLILL 9

RESULT 31

S40313
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40313
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40313
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-123 <KLB>
 A/Cross-references: EMBL:X72423; NID:G441314; PIDN:CAAS1091.1; PID:G441315
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LIGLILL 10
 |||||
 Db 3 LIGLILL 9

RESULT 32
 S40354
 Ig kappa chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40354
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40354
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-123 <KLB>
 A/Cross-references: EMBL:X72464; NID:G441396; PIDN:CAAS1132.1; PID:G441397
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/30-104/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LIGLILL 10
 |||||
 Db 1 LIGLILL 7

RESULT 33
 S40318
 Ig kappa chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40318
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40318
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-124 <KLB>
 A/Cross-references: EMBL:X72428; NID:G441324; PIDN:CAAS1096.1; PID:G441325
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
 |||||
 Db 3 LIGLILL 9

RESULT 34
 S40336
 Ig kappa chain V-J region - human
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40336
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40336
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-124 <KLB>
 A/Cross-references: EMBL:X72446; NID:G441360; PIDN:CAAS1114.1; PID:G441361
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/31-105/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LIGLILL 10
 |||||
 Db 2 LIGLILL 8

RESULT 35
 S40348
 Ig kappa chain V-J region - human
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40348
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40348
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-124 <KLB>
 A/Cross-references: EMBL:X72458; NID:G441384; PIDN:CAAS1126.1; PID:G441385
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LIGLILL 10
 |||||
 Db 7 LIGLILL 13

RESULT 36
 S04936
 Ig kappa chain precursor V-J region (1H1) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 26-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
 C/Accession: S04936
 R/Levy, S.; Mendel, E.; Kon, S.; Avnur, Z.; Levy, R.
 J. Exp. Med. 168, 475-489, 1988
 A/Title: Mutational hot spots in Ig V region genes of human follicular lymphomas.
 A/Reference number: S04936; MUID:88316166; PMID:3045247
 A/Accession: S04936

A:Molecule type: mRNA
A:Residues: 1-125 <LEU>
A:Cross-references: EMBL:X13076; NID:G33173; PIDN:CAA11477.1; PID:G736243
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F:18-125/Product: Ig kappa chain (fragment) #status predicted <MAT>
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
DB 4 LIGLILL 10

RESULT 37

S40353
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 13-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40353
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40353
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLB>
A:Cross-references: EMBL:X72463
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
DB 1 LIGLILL 7

RESULT 38

S40333
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40333
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40333
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLB>
A:Cross-references: EMBL:X72443; NID:G441354; PIDN:CA51111.1; PID:G441355
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
DB 5 LIGLILL 11

RESULT 39

S40316
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40316
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40316
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLB>
A:Cross-references: EMBL:X72426
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
DB 2 LIGLILL 8

RESULT 40

S40349
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S40349
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40349
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLB>
A:Cross-references: EMBL:X72459; NID:G441386; PIDN:CA51127.1; PID:G441387
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
DB 4 LIGLILL 10

RESULT 41

S40315
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40315
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40315
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLB>
A:Cross-references: EMBL:X72425; NID:G441318; PIDN:CA51093.1; PID:G441319
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
DB 2 LIGLILL 8

RESULT 42

E70420
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain nuoA1 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C;Accession: E70420
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.B.; O'V.
Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Accession: E70420
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-126 <AQF>
A;Cross-references: UNIPROT:O67392; GB:AE000737; NID:92983782; PIDN:AA07346.1; PID:9298

A;Experimental source: strain VFS
C;Genetics:
A;Gene: nuoA1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 3

C;Keywords: membrane-associated complex; NAD; oxidoreductase
Query Match 2.2%; Score 7; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
DB 64 LIGLILL 70

RESULT 43

S40335
Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40335
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40335
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-126 <KLE>

A;Cross-references: EMBL:X72445
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
DB 2 LIGLILL 8

RESULT 44

S40367
Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40367
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40367
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-127 <KLE>

A;Cross-references: EMBL:X72477
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-107/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
DB 4 LIGLILL 10

RESULT 45
S11240
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S11240
R;Feigenhauer, M.; Kohl, U.; Rueker, F.
Nucleic Acids Res. 18, 4927, 1990

A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
A;Reference number: S11239; MUID:90370490; PMID:1697678

A;Accession: S11240
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-127 <FEL>

A;Cross-references: EMBL:X53612; NID:923868; PIDN:CAA37674.1; PID:9762937
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
DB 9 LIGLILL 15

RESULT 46
A23986
Ig kappa chain precursor V region (IR162) - rat
C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change 21-Jan-2000
C;Accession: A23986
R;Helman, L.; Engstrom, A.; Bennich, H.; Petersson, U.
Gene 40, 107-114, 1985

A;Title: Structure and expression of kappa-chain genes in two IgB-producing rat immuno-
A;Reference number: A91541; MUID:86137406; PMID:3005117

A;Accession: A23986
A;Molecule type: mRNA
A;Residues: 1-127 <HEL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 7 LIGLILL 13

RESULT 47

S46372
IG light chain variable region (VC) - human
C/Species: Homo sapiens (man)
C/Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C/Accession: S46372
R/Bensimon, C.; Chaetagner, P.; Zouali, M.
EMBL J. 13, 2951-2962, 1994
A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chI) gene re-
A/Reference number: S46369; MUID:94313975; PMID:8039491
A/Accession: S46372
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-128 <BEN>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 7 LIGLILL 13

RESULT 48

KIRHDI
Ig kappa chain precursor V-I region (Daudi) - human
C/Species: Homo sapiens (man)
C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C/Accession: A01884
R/Klobeck, H.G.; Combrat, G.; Zachau, H.G.
Nucleic Acids Res. 12, 6995-7006, 1984
A/Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell
A/Reference number: A93534; MUID:85014148; PMID:6091049
A/Accession: A01884
A/Molecule type: DNA
A/Residues: 1-129 <KLO>
A/Cross-references: UNIPROT:P04432; GB:K02134; NID:g185821; PID:g185822
A/Note: the sequence was determined from the differentiated gene
C/Genetics:
A/Gene: GDB:IGKV1
A/Cross-references: GDB:136264
A/Map position: 2p12-2p12
A/Intons: 19/1
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-129/Product: Ig kappa chain V-I region (Daudi) #status predicted <MAY>
F/23-129/Region: framework 1
F/23-45/Region: framework 2
F/38-112/Domain: immunoglobulin homology <IMM>
F/46-56/Region: complementarity-determining 1
F/57-71/Region: framework 2
F/72-78/Region: complementarity-determining 2
F/79-110/Region: framework 3
F/111-119/Region: complementarity-determining 3
F/120-129/Region: framework 4
F/45-110/Disulfide bonds: #status predicted

Query Match 2.2%; Score 7; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 9 LIGLILL 15

RESULT 49

KIRHMK
Ig kappa chain precursor V-I region (Walker) - human
C/Species: Homo sapiens (man)
C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C/Accession: A01883
R/Klobeck, H.G.; Combrat, G.; Zachau, H.G.
Nucleic Acids Res. 12, 6995-7006, 1984
A/Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cel
A/Reference number: A93534; MUID:85014148; PMID:6091049
A/Accession: A01883
A/Molecule type: DNA
A/Residues: 1-129 <KLO>
A/Cross-references: UNIPROT:P04431
A/Note: the sequence was determined from the differentiated gene
C/Genetics:
A/Gene: GDB:IGKV1
A/Cross-references: GDB:136264
A/Map position: 2p12-2p12
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-129/Product: Ig kappa chain V-I region (Walker) #status predicted <MAY>
F/23-45/Region: framework 1
F/38-112/Domain: immunoglobulin homology <IMM>
F/46-56/Region: complementarity-determining 1
F/57-71/Region: framework 2
F/72-78/Region: complementarity-determining 2
F/79-110/Region: framework 3
F/111-119/Region: complementarity-determining 3
F/120-129/Region: framework 4
F/45-110/Disulfide bonds: #status predicted

Query Match 2.2%; Score 7; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 9 LIGLILL 15

RESULT 50

S52789
Ig kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C/Accession: S52789
R/Rocca, A.; Khanlidi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret
submitted to the EMBL Data Library, March 1995
A/Description: Light chain V region gene usage restriction and peculiarities in myeloma
A/Reference number: S52789
A/Accession: S52789
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-129 <ROC>
A/Cross-references: EMBL:X85995; NID:g758588; PID:CA55987.1; PID:g758589
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LIGLILL 10
| | | | |
Db 9 LIGLILL 15

RESULT 51

S52792

Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000

C/Accession: S52792

R/Rocca, A.; Khamlich, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,

submitted to the EMBL Data Library, March 1995

A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-

A:Reference number: S52789

A:Accession: S52792

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-129 <KLE>

A:CROSS-references: EMBL:X85996; NID:G758598; PIDN:CAAS9988.1; PID:G758599

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LIGLILL 10
| | | | |
Db 9 LIGLILL 15

RESULT 52

S40317

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40317

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40317

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-129 <KLE>

A:CROSS-references: EMBL:X72427; NID:G441322; PIDN:CAAS1095.1; PID:G441323

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LIGLILL 10
| | | | |
Db 8 LIGLILL 14

RESULT 53

S52793

Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000

C/Accession: S52793

R/Rocca, A.; Khamlich, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,

submitted to the EMBL Data Library, March 1995

A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-

A:Reference number: S52789

A:Accession: S52793

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:CROSS-references: EMBL:X85997; NID:G758600; PIDN:CAAS9989.1; PID:G758601
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LIGLILL 10
| | | | |
Db 9 LIGLILL 15

RESULT 54

S40369

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40369

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40369

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-129 <KLE>

A:CROSS-references: EMBL:X72479; NID:G441426; PIDN:CAAS1147.1; PID:G441427

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LIGLILL 10
| | | | |
Db 8 LIGLILL 14

RESULT 55

S40332

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40332

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40332

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-129 <KLE>

A:CROSS-references: EMBL:X72442; NID:G441352; PIDN:CAAS1110.1; PID:G441353

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LIGLILL 10
| | | | |
Db 4 LIGLILL 10

RESULT 56
PL0113
Ig kappa chain precursor V-I region (CJ) - human
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C/Accession: PL0113
R/Levy, S.; Mendel, E.; Kon, S.; Avnur, Z.; Levy, R.
J. Exp. Med. 168, 475-489, 1988
A/Title: Mutational hot spots in Ig V region genes of human follicular lymphomas.
A/Reference number: S04936; MUID:8831616; PMID:3045247
A/Accession: PL0113
A/Molecule type: mRNA
A/Residues: 1-130 <LEV>
A/Experimental source: follicular lymphoma cells
A/Note: the sequence shown here is derived from the consensus nucleotide sequence of the
om tumor cells of a single patient
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; hybridoma; immunoglobulin
F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-130/Product: Ig kappa chain V-I region CJ #status predicted <MAT>
F/38-112/Domain: immunoglobulin homology <IMM>
F/46-56/Region: complementarity-determining 1
F/72-78/Region: complementarity-determining 2
F/111-130/Region: complementarity-determining 3
F/118-130/Region: J1

Query Match 2.2%; Score 7; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 9 LIGLILL 15

RESULT 57
S40368
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40368
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40368
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-130 <KLB>
A/Cross-references: EMBL:X72478; NID:G441424; PIDN:CAAS1146.1; PID:G441425
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 4 LIGLILL 10

RESULT 58
S08079
Ig kappa chain precursor V-J region (clone VKB95g) - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Jan-2000
C/Accession: S08079
R/Myadi, H.; Cazenave, P.A.; Marche, P.N.
submitted to the EMBL Data Library, February 1989
A/Reference number: S08077
A/Accession: S08079

A/Molecule type: DNA
A/Residues: 1-130 <AYA>
A/Cross-references: EMBL:X14364
C/Genetics: 17/3
A/Intons: 17/3
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/1-17/Domain: signal sequence #status predicted <SIG>
F/18-113/Product: Ig kappa chain (fragment) #status predicted <MAT>
F/38-113/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 9 LIGLILL 15

RESULT 59
S40352
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40352
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40352
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-131 <KLB>
A/Cross-references: EMBL:X72462; NID:G441392; PIDN:CAAS1130.1; PID:G441393
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 7 LIGLILL 13

RESULT 60
S38646
Ig kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S38646
R/Bensimon, C.; Chastagner, P.; Zouali, M.
submitted to the EMBL Data Library, November 1993
A/Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A/Reference number: S38643
A/Accession: S38646
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-132 <BEN>
A/Cross-references: EMBL:Z27173; NID:G415961; PIDN:CAAS1697.1; PID:G415962
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/40-114/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||

Db 11 LIGLILL 17

RESULT 61

S40334

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40334

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40334

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-132 <KLE>

A:Cross-references: EMBL:X72444

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 8 LIGLILL 14

RESULT 62

S24320

Ig kappa chain precursor - human

C:Species: Homo sapiens (man)

C>Date: 02-Dec-1993 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000

C:Accession: S24320

R:Aucuturier, P.; Khamlich, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Cogne,

Biochem. J. 285, 149-152, 1992

A:Title: Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain pr

A:Reference number: S24319; MUID:92344562; PMID:1379039

A:Accession: S24320

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-135 <AUC>

A:Cross-references: EMBL:X64133; NID:932810; PIDN:CAA45494.1; PID:932811

A>Note: the authors translated the codon CAA for residue 122 as Glu

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 9 LIGLILL 15

RESULT 63

S40365

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40365

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40365

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-139 <KLE>

A:Cross-references: EMBL:X72475; NID:9441418; PIDN:CAA51143.1; PID:9441419

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 2 LIGLILL 8

RESULT 64

A49134

Ig kappa chain V-I region (ISE) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C:Accession: A49134; S25115

R:Rocca, A.; Khamlich, A.A.; Aucuturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, J.

Clin. Exp. Immunol. 91, 506-509, 1993

A:Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in 11g

A:Reference number: A49134; MUID:93185310; PMID:7680298

A:Accession: A49134

A:Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-141 <ROC>

A:Cross-references: EMBL:X67322; NID:933268; PIDN:CAA47736.1; PID:933269

A>Note: sequence extracted from NCBI backbone (NCBI:P:127088)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 9 LIGLILL 15

RESULT 65

S57086

YAK1 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein J1805; protein YOR067c

C:Species: Saccharomyces cerevisiae

C>Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004

C:Accession: S57086; S71689

R:Manus, V.; Huang, M.E.; Galibert, F.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S57085

A:Accession: S57086

A:Molecule type: DNA

A:Residues: 1-141 <MAN>

A:Cross-references: UNIPROT:P47118; EMBL:Z49567; NID:91015744; PID:91015745; MIPS:YOR06

R:Huang, M.E.; Manus, V.; Chuat, J.C.; Galibert, F.

Yeast 12, 869-875, 1996

A:Title: Analysis of a 62 kb DNA sequence of chromosome X reveals 36 open reading frame

A:Reference number: S71676; MUID:96437976; PMID:8840504

A:Accession: S71689

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Cross-references: EMBL:L47993; NID:91019675; PIDN:AA839293.1; PID:91019689

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995

C:Genetics:

A:Gene: SGD:YAK1

A:Cross-references: SGD:S0003828; MIPS:YOR067c

A:Map position: 10R

Query Match 2.2%; Score 7; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLIG 7
|||||
DB 69 MGILLIG 75

RESULT 66
T45630
hypothetical protein F13G24.250 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C/Accession: T45630
R/Revan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba
submitted to the Protein Sequence Database, December 1999
A/Reference number: Z23009
A/Accession: T45630
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1158 <REV>
A/Cross-references: UNIPROT:Q9SDJ9; EMBL:AL133421
A/Experimental source: cultivar Columbia; BAC clone F13G24
C/Genetics:
A/Map position: 5
A/Introns: 33/3
A/Note: F13G24.250

Query Match 2.2%; Score 7; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LGILLIG 11
|||||
DB 106 LGILLIG 112

RESULT 67
D95096
hemolysin-related protein [imported] - Streptococcus pneumoniae (strain TIGR4)
C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C/Accession: D95096
R/Rettelin, H.; Nelson, K.R.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umeyam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A/Reference number: A95000; PMID:21357209; PMID:11463916
A/Accession: D95096
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-170 <KUR>
A/Cross-references: UNIPROT:Q97R11; GB:AE005672; PIDN:AAK74965.1; PID:G14972307; GSPDB:C
A/Experimental source: strain TIGR4
C/Genetics:
A/Gene: SP0834

Query Match 2.2%; Score 7; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 DGNQVVR 127
|||||
DB 87 DGNQVVR 93

RESULT 68
A97964
conserved hypothetical protein, truncation spr0737 [imported] - Streptococcus pneumoniae
C/Species: Streptococcus pneumoniae

C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: A97964
R/Hoskins, J.A.; Albom Jr., W.; Arnold, J.; Blaszcak, L.; Buggett, S.; Dehoff, B.S.;
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McHenry, S.;
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; PMID:21429245; PMID:11544234
A/Accession: A97964
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-170 <KUR>
A/Cross-references: UNIPROT:Q9DQC9; GB:AE007317; PIDN:AAK99541.1; PID:G15458330; GSPDB:C
C/Genetics:
A/Gene: spr0737

Query Match 2.2%; Score 7; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 DGNQVVR 127
|||||
DB 87 DGNQVVR 93

RESULT 69
I53285
glucocorticoid-regulated endocrine protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C/Accession: I53285
R/Bloomquist, B.T.; Darlington, D.N.; Mueller, G.P.; Mains, R.E.; Eipper, B.A.
Endocrinology 135, 2714-2722, 1994
A/Title: Regulated endocrine-specific protein-18: a short-lived novel glucocorticoid-re
A/Reference number: I53285; PMID:95080145; PMID:798462
A/Accession: I53285
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-175 <RES>
A/Cross-references: UNIPROT:P47939; GB:I34214; NID:G609540; PIDN:AAA67425.1; PID:G609541
C/Genetics:
A/Gene: RESP18

Query Match 2.2%; Score 7; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 GQGVSRQ 221
|||||
DB 39 GQGVSRQ 45

RESULT 70
A53523
endocrine secretory protein RESP18 precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C/Accession: A53523
R/Bloomquist, B.T.; Darlington, D.N.; Mains, R.E.; Eipper, B.A.
J. Biol. Chem. 269, 9113-9122, 1994
A/Title: RESP18, a novel endocrine secretory protein transcript, and four other transcr
A/Reference number: A53523; PMID:94179330; PMID:8132649
A/Accession: A53523
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-175 <BLO>
A/Cross-references: UNIPROT:P47940; GB:I25633; NID:G468923; PIDN:AAB59694.1; PID:G46892
C/Keywords: endoplasmic reticulum; polymorphism

Query Match 2.2%; Score 7; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 215 GOWSEQ 221
 Db 39 GOWSEQ 45

RESULT 71

AI0676
 Probable exported protein STY1533 [imported] - *Salmonella enterica* subsp. *enterica* serov. *Paratyphi*
 C:Species: *Salmonella enterica* subsp. *enterica* serovar *Typhi*
 A:Note: this species has also been called *Salmonella typhi*
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AI0676
 R:Perkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; Connetton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov. *Paratyphi*
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AI0676
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-180 <PAR>
 A:Cross-references: GB:AL513382; PTDN:CAD01786.1; PTD:gl6502631; GSPDB:GN00176
 C:Genetic81
 A:Gene: STY1533

Query Match 2.2% Score 7/ DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 253 ATSTVKQ 259
 Db 39 ATSTVKQ 45

RESULT 72

H84273
 Flagellin A1 precursor [imported] - *Halobacterium* sp. NRC-1
 C:Species: *Halobacterium* sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: H84273
 R:Ng, W.V.; Kennedy, S.P.; Mahapatra, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leitauer, B.; Keller, K.; Cruz, R.; Danson, M.W.; Hough, D.W.; Maddocks, D.G.; Jablo, Jung, K.H.; Alam, M.; Freilich, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li, A:Title: Genome sequence of *Halobacterium* species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: H84273
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-207 <STO>
 A:Cross-references: UNIRROT:QHQF9; GB:AE004437; NTD:gl0580714; PTDN:AMG19556.1; GSPDB:C
 C:Genetic81
 A:Gene: FlaA1b
 C:Superfamily: archaeal flagellin

Query Match 2.2% Score 7/ DB 2; Length 207;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 VPESVTG 31
 Db 195 VPESVTG 201

RESULT 73

IG2056
 Ig kappa chain precursor V-J-C regions - rabbit (fragment)
 C:Species: *Oryctolagus cuniculus* (domestic rabbit)
 C:Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000

C:Accession: A20969; A25448
 R:McCartney-Francis, N.; Skurja Jr., R.M.; Mage, R.G.; Bernstein, K.B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 1794-1798, 1984
 A:Title: Kappa-chain allotypes and isotypes in the rabbit: cDNA sequences of clones encoding type expression.
 A:Reference number: A20969; MUID:84170388; PMID:6424124
 A:Accession: A20969
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-229 <MCC>
 A:Cross-references: GB:G01359; NID:gl65373; PTDN:AAA31334.1; PID:gl65374
 R:Aikman, M.A.; Mariani, B.; Rougeon, F.
 Proc. Natl. Acad. Sci. U.S.A. 83, 5180-5183, 1986
 A:Title: Evolution of the immunoglobulin kappa light chain locus in the rabbit: evidence
 A:Reference number: A94110; MUID:86259753; PMID:3088570
 A:Contents: Ig kappa-1 chain, 69 allotype, J-K1.2 segment
 A:Accession: A25448
 A:Molecule type: DNA
 A:Residues: 111-123 <AKT>

A:Cross-references: GB:M14067; GB:M14062; GB:M14063; GB:M14064; GB:M14065; GB:M14066; N
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:143-212/Domain: immunoglobulin homology <IMM>

Query Match 2.2% Score 7/ DB 2; Length 229;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LIGLILL 10
 Db 1 LIGLILL 7

RESULT 74

S33161
 Ig kappa chain - sheep
 C:Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S33161
 R:Foley, R.C.; Beh, K.J.
 Submitted to the EMBL Data Library, July 1990
 A:Description: Isolation and characterization of sheep kappa light chain cDNA.
 A:Reference number: S33161
 A:Accession: S33161
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-230 <FOL>
 A:Cross-references: EMBL:X54110; NID:G297103; PTDN:CAA38046.1; PID:gl364221
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:143-212/Domain: immunoglobulin homology <IMM>

Query Match 2.2% Score 7/ DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LIGLILL 10
 Db 2 LIGLILL 8

RESULT 75

JU0284
 Fc gamma (IgG) receptor III-B precursor (neutrophil) - human
 N:Alternate names: FcR III; IgG Fc receptor precursor, type III-1 (polymorphonuclear gr
 C:Species: *Homo sapiens* (man)
 C:Date: 07-Sep-1990 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C:Accession: JU0284; S00758; J37628; B32933; A31460
 R:Ravetch, J.V.; Perussia, B.
 J. Exp. Med. 170, 481-497, 1989
 A:Title: Alternative membrane forms of Fc gamma RIII (CD16) on human natural killer cell
 A:Reference number: J10107; MUID:89328325; PMID:2526846
 A:Accession: JU0284

```

A:Molecule type: mRNA
A:Residues: 1-201,'SF',204-233 <RAV>
A:Cross-references: UNIPROT:O75015; GB:J04162
A>Note: the sequence of the receptor from human NK cells, reported in the same paper, differs by 1 end
R:Simmons, D.; Seed, B.
Nature 333, 568-570, 1998
A>Title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membrane protein
A:Reference number: S00758; MIMD:88232937; PMID:2967436
A:Accession: S00758
A:Molecule type: mRNA
A:Residues: 1-233 <SIM>
A:Cross-references: EMBL:X07934; NID:G29744; PIDN:CAA30758.1; PID:G29745
R:Gesener, J.E.; Grussemeyer, T.; Kolanus, W.; Schmidt, R.E.
J. Biol. Chem. 270, 1350-1361, 1995
A>Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole
A:Reference number: A55439; MIMD:9518131; PMID:7836402
A:Accession: I37628
A:Molecule type: DNA
A:Residues: 1-72 <RRS>
A:Cross-references: EMBL:Z46223; NID:G559446; PIDN:CAA86296.1; PID:G871306
R:Scallion, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeles, J.C.
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989
A>Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phos
A:Reference number: A32933; MIMD:8926947; PMID:2525780
A:Accession: B32933
A:Molecule type: mRNA
A:Residues: 1-121,'E',123-150,'S',152-233 <SCA>
A:Cross-references: GB:M24854; NID:G184851; PIDN:AA53507.1; PID:G306930
R:Peltz, G.A.; Grundy, H.O.; Lebo, R.V.; Yseel, H.; Barsh, G.S.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 1013-1017, 1989
A>Title: Human Fc-gamma-RIII: cloning, expression, and identification of the chromosomal
A:Reference number: A31460; MIMD:89128838; PMID:2521732
A:Accession: A31460
A:Molecule type: mRNA
A:Residues: 1-35,'R',37-64,'N',66-81,'D',83-105,'V',107-233 <PEL>
A:Cross-references: GB:J04162; NID:G183036; PIDN:AA35881.1; PID:G183037
C:Comment: This low affinity IgG Fc receptor of neutrophils, which is the product of the
1, yet this receptor lacks 21 residues at the carboxyl end because of an early stop cod
C:Genetics:
A:Gene: GDB:FCGR3B; FCGR3; FCGR3
A:Cross-references: GDB:128176; OMIM:146740
A:Map position: 1q23-1q23
A:Introns: 14/1; 21/1
A>Note: the list of introns is incomplete
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkage
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-203/Product: Fc gamma (IgG) receptor IIR-B #status predicted <MAT>
F:40-91/Domain: immunoglobulin homology <IMM1>
F:111-174/Domain: immunoglobulin homology <IMM2>
F:56,63,82,92,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:203/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form)

Query Match          2.2%; Score 7; DB 1; Length 233;
Best local similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      205 DSGSYFC 211
        |||||
        |||||
DB      166 DSGSYFC 172

Search completed: January 4, 2005, 07:00:38
Job time : 30 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 06:07:15, Search time 27 Seconds

(without alignments)
788.447 Million cell updates/sec

Title: US-10-767-374-2

Perfect score: 1688
Sequence: 1 MGILLGLLGLHITVDYGR.....AYIMCKRTSQGHVYEAAR 321

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database:

Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCURS.COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1688	100.0	321	4	US-09-254-465A-2
2	1137	67.4	306	4	US-09-369-247-63
3	178.5	10.6	299	3	US-09-188-930-189
4	178.5	10.6	299	3	US-09-188-930-331
5	178.5	10.6	299	3	US-09-462-270-2
6	178.5	10.6	299	3	US-09-254-465A-1
7	178.5	10.6	299	4	US-09-312-283C-189
8	178.5	10.6	299	4	US-09-312-283C-331
9	178.5	10.6	299	4	US-09-907-794A-119
10	178.5	10.6	299	4	US-09-907-794A-119
11	178.5	10.6	299	4	US-09-907-794A-119
12	178.5	10.6	299	4	US-09-397-243D-3
13	178.5	10.6	299	4	US-09-906-700-119
14	178.5	10.6	299	4	US-10-140-002-166
15	178.5	10.6	299	4	US-09-903-603A-119
16	177	10.5	319	1	US-08-597-495B-22
17	177	10.5	319	1	US-08-597-495B-22
18	177	10.5	319	3	US-09-068-051A-22
19	177	10.5	319	4	US-09-336-536-67
20	176	10.4	270	4	US-09-254-465A-6
21	176	10.4	273	4	US-09-254-465A-24
22	172.5	10.2	316	4	US-09-397-243D-13
23	169.5	10.0	260	4	US-09-254-465A-23
24	169.5	10.0	263	4	US-09-254-465A-25
25	167	9.9	300	4	US-09-254-465A-10
26	167	9.9	300	4	US-09-397-243D-12
27	166	9.8	365	4	US-09-899-634C-4

28	163.5	9.7	261	4	US-09-899-634C-2	Sequence 2, App1
29	161.5	9.6	318	3	US-09-068-051A-32	Sequence 32, App1
30	158	9.4	365	2	US-08-979-424-3	Sequence 3, App1
31	158	9.4	365	3	US-08-928-383B-2	Sequence 2, App1
32	158	9.4	365	3	US-09-272-196-2	Sequence 2, App1
33	153.5	9.1	373	4	US-10-140-002-388	Sequence 388, App
34	151	8.9	466	4	US-09-604-107A-8	Sequence 8, App1
35	142.5	8.4	398	4	US-09-778-510-4	Sequence 4, App1
36	141.5	8.4	1395	3	US-09-540-245A-15	Sequence 15, App1
37	140.5	8.3	365	3	US-08-928-383B-23	Sequence 23, App1
38	140.5	8.3	365	3	US-08-928-383B-24	Sequence 24, App1
39	140.5	8.3	365	3	US-08-928-383B-26	Sequence 26, App1
40	138.5	8.2	310	4	US-09-307-794A-423	Sequence 423, App
41	138.5	8.2	310	4	US-09-307-794A-423	Sequence 423, App
42	138.5	8.2	310	4	US-09-307-794A-423	Sequence 423, App
43	138.5	8.2	310	4	US-09-307-794A-423	Sequence 423, App
44	138.5	8.2	310	4	US-10-140-002-538	Sequence 538, App
45	138.5	8.2	310	4	US-09-503-603A-423	Sequence 423, App
46	138.5	8.2	360	4	US-09-907-794A-213	Sequence 213, App
47	138	8.2	360	4	US-09-907-794A-213	Sequence 213, App
48	138	8.2	360	4	US-09-907-794A-213	Sequence 213, App
49	138	8.2	360	4	US-09-907-794A-213	Sequence 213, App
50	138	8.2	360	4	US-09-907-794A-213	Sequence 213, App
51	136	8.1	205	3	US-09-462-270-4	Sequence 42, App1
52	135	8.0	249	4	US-09-336-536-42	Sequence 42, App1
53	135	8.0	394	4	US-09-336-536-39	Sequence 39, App1
54	134.5	8.0	133	4	US-09-397-243D-4	Sequence 4, App1
55	134.5	8.0	450	4	US-09-907-794A-320	Sequence 320, App
56	134.5	8.0	450	4	US-09-505-125A-320	Sequence 320, App
57	134.5	8.0	450	4	US-09-505-125A-320	Sequence 320, App
58	134.5	8.0	450	4	US-09-505-125A-320	Sequence 320, App
59	134.5	8.0	450	4	US-10-140-002-378	Sequence 378, App
60	134.5	8.0	450	4	US-09-903-603A-320	Sequence 320, App
61	134	7.9	440	3	US-08-759-628-4	Sequence 4, App1
62	133.5	7.9	398	4	US-09-778-510-6	Sequence 6, App1
63	133.5	7.9	398	4	US-09-907-794A-84	Sequence 84, App1
64	133.5	7.9	398	4	US-09-905-125A-84	Sequence 84, App1
65	133.5	7.9	398	4	US-09-906-700-84	Sequence 84, App1
66	133.5	7.9	398	4	US-09-906-700-84	Sequence 84, App1
67	133.5	7.9	398	4	US-10-140-002-348	Sequence 348, App1
68	133.5	7.9	398	4	US-09-903-603A-84	Sequence 84, App1
69	133.5	7.9	432	4	US-09-778-510-2	Sequence 2, App1
70	133	7.9	561	4	US-09-866-510-24	Sequence 24, App1
71	133	7.9	1059	4	US-09-907-794A-290	Sequence 290, App
72	133	7.9	1059	4	US-09-905-125A-290	Sequence 290, App
73	133	7.9	1059	4	US-09-902-775A-290	Sequence 290, App
74	133	7.9	1059	4	US-09-906-700-290	Sequence 290, App
75	133	7.9	1059	4	US-09-903-603A-290	Sequence 290, App
76	133	7.9	1059	4	US-09-866-510-14	Sequence 14, App1
77	133	7.9	1106	1	US-08-180-195-2	Sequence 2, App1
78	133	7.9	1106	1	US-08-168-517-2	Sequence 2, App1
79	133	7.9	1106	1	US-08-477-329-2	Sequence 2, App1
80	133	7.9	1106	2	US-08-475-458-2	Sequence 2, App1
81	133	7.9	1106	2	US-08-460-510-2	Sequence 2, App1
82	133	7.9	1106	2	US-08-460-510-2	Sequence 2, App1
83	133	7.9	1106	2	US-08-980-400-2	Sequence 2, App1
84	133	7.9	1106	3	US-08-462-728-4	Sequence 4, App1
85	133	7.9	1106	3	US-09-583-459A-2	Sequence 2, App1
86	133	7.9	1106	3	US-09-583-459A-2	Sequence 2, App1
87	133	7.9	1106	3	US-09-583-459A-2	Sequence 2, App1
88	133	7.9	1106	3	US-09-583-459A-2	Sequence 2, App1
89	133	7.9	1106	3	US-09-435-059-2	Sequence 2, App1
90	133	7.9	1106	3	US-08-461-817-4	Sequence 4, App1
91	133	7.9	1106	4	US-08-464-436-4	Sequence 4, App1
92	133	7.9	1106	4	US-09-866-510-16	Sequence 16, App1
93	133	7.9	1106	4	US-09-866-510-18	Sequence 18, App1
94	133	7.9	1106	4	US-09-866-510-22	Sequence 22, App1
95	133	7.9	1106	4	US-09-866-510-22	Sequence 22, App1
96	133	7.9	1106	5	PCT-US92-00730-2	Sequence 2, App1
97	133	7.9	1106	5	PCT-US92-00862-2	Sequence 2, App1
98	133	7.9	1119	4	US-09-907-794A-294	Sequence 294, App
99	133	7.9	1119	4	US-09-905-125A-294	Sequence 294, App
100	133	7.9	1119	4	US-09-902-775A-294	Sequence 294, App

101	133	7.9	1119	4	US-09-906-700-294	Sequence 294, App
102	133	7.9	1119	4	US-10-140-002-352	Sequence 352, App
103	133	7.9	1119	4	US-09-903-603A-294	Sequence 294, App
104	132.5	7.8	630	2	US-08-752-307B-14	Sequence 14, App1
105	132.5	7.8	630	3	US-09-707-802-14	Sequence 14, App1
106	132.5	7.8	630	3	US-09-991-326-14	Sequence 14, App1
107	127	7.5	227	4	US-09-205-258-947	Sequence 947, App
108	127	7.5	462	2	US-08-752-307B-7	Sequence 7, App1
109	127	7.5	462	3	US-09-707-802-7	Sequence 7, App1
110	127	7.5	462	3	US-09-991-326-7	Sequence 7, App1
111	127	7.5	465	2	US-08-752-307B-5	Sequence 5, App1
112	127	7.5	465	3	US-09-707-802-5	Sequence 5, App1
113	127	7.5	465	3	US-09-991-326-5	Sequence 5, App1
114	126.5	7.5	924	1	US-08-481-130-28	Sequence 28, App1
115	126.5	7.5	924	1	US-08-656-984A-28	Sequence 28, App1
116	126.5	7.5	924	1	US-08-485-604-28	Sequence 28, App1
117	126.5	7.5	924	2	US-08-487-595-28	Sequence 28, App1
118	124.5	7.4	397	4	US-09-175-928-2	Sequence 2, App1
119	123	7.3	313	4	US-09-700-397-4	Sequence 4, App1
120	123	7.3	344	4	US-09-700-397-3	Sequence 3, App1
121	123	7.3	344	4	US-10-140-002-376	Sequence 376, App
122	122.5	7.3	612	2	US-08-752-307B-11	Sequence 11, App1
123	122.5	7.3	612	3	US-09-707-802-11	Sequence 11, App1
124	122.5	7.3	612	3	US-09-991-326-11	Sequence 11, App1
125	122.5	7.3	1268	3	US-08-506-296B-28	Sequence 28, App1
126	122	7.2	611	2	US-08-752-307B-10	Sequence 10, App1
127	122	7.2	611	2	US-09-707-802-10	Sequence 10, App1
128	122	7.2	611	3	US-09-991-326-10	Sequence 10, App1
129	120.5	7.1	373	4	US-09-823-038A-60	Sequence 60, App1
130	120.5	7.1	440	4	US-09-866-028-61	Sequence 61, App1
131	120.5	7.1	440	4	US-09-944-457-61	Sequence 61, App1
132	120.5	7.1	442	4	US-09-778-510-20	Sequence 20, App1
133	120.5	7.1	442	4	US-09-930-803-1	Sequence 1, App1
134	120.5	7.1	529	3	US-09-383-586-31	Sequence 31, App1
135	120.5	7.1	529	4	US-09-823-038A-31	Sequence 31, App1
136	120	7.1	312	4	US-09-254-665A-9	Sequence 9, App1
137	120	7.1	312	4	US-09-907-794A-64	Sequence 64, App1
138	120	7.1	312	4	US-09-905-125A-64	Sequence 64, App1
139	120	7.1	312	4	US-09-902-775A-64	Sequence 64, App1
140	120	7.1	312	4	US-09-906-770A-64	Sequence 64, App1
141	120	7.1	312	4	US-10-140-002-336	Sequence 336, App
142	120	7.1	312	4	US-09-903-603A-64	Sequence 64, App1
143	120	7.1	1101	3	US-08-986-485-2	Sequence 2, App1
144	119.5	7.1	298	4	US-09-152-060-76	Sequence 76, App1
145	119.5	7.1	464	2	US-08-602-725-32	Sequence 32, App1
146	119.5	7.1	467	3	US-09-046-736-2	Sequence 40, App1
147	119	7.0	365	4	US-09-336-536-40	Sequence 40, App1
148	119	7.0	1091	3	US-08-986-485-5	Sequence 5, App1
149	118.5	7.0	321	6	5169835-17	Patent No. 5169835
150	118	7.0	518	3	US-09-240-915-8	Sequence 8, App1
151	118	7.0	518	3	US-09-591-435-8	Sequence 8, App1
152	118	7.0	547	1	US-08-474-981A-6	Sequence 6, App1
153	118	7.0	547	2	US-08-474-087-6	Sequence 6, App1
154	118	7.0	758	2	US-08-874-678-1	Sequence 1, App1
155	118	7.0	758	3	US-08-643-839-1	Sequence 1, App1
156	118	7.0	758	3	US-09-051-363-24	Sequence 24, App1
157	118	7.0	758	3	US-09-348-886-14	Sequence 14, App1
158	118	7.0	780	1	US-08-232-538-14	Sequence 14, App1
159	118	7.0	780	2	US-08-786-164-14	Sequence 14, App1
160	118	7.0	1338	3	US-08-750-0141A-3	Sequence 3, App1
161	118	7.0	1338	4	US-09-119-014D-6	Sequence 6, App1
162	117.5	7.0	308	2	US-08-414-657D-46	Sequence 46, App1
163	117.5	7.0	325	2	US-08-414-657D-2	Sequence 2, App1
164	117.5	7.0	325	2	US-08-414-657D-41	Sequence 41, App1
165	117.5	7.0	325	2	US-09-135-080-2	Sequence 2, App1
166	117.5	7.0	338	4	US-08-414-657D-60	Sequence 60, App1
167	117.5	7.0	338	4	US-09-135-080-8	Sequence 8, App1
168	117.5	7.0	338	4	US-09-976-594-404	Sequence 404, App
169	117.5	7.0	615	2	US-08-752-307B-9	Sequence 9, App1
170	117.5	7.0	615	2	US-09-707-802-9	Sequence 9, App1
171	117.5	7.0	615	3	US-09-991-326-9	Sequence 9, App1
172	117	6.9	292	4	US-09-800-729-175	Sequence 175, App
173	117	6.9	1447	3	US-09-041-886-25	Sequence 25, App1
174	117	6.9	1447	5	PCT-US94-05277-2	Sequence 2, App1
175	117	6.9	1745	2	US-09-800-729-89	Sequence 89, App1
176	116.5	6.9	315	2	US-08-414-657D-47	Sequence 47, App1
177	116.5	6.9	338	2	US-08-414-657D-42	Sequence 42, App1
178	116.5	6.9	338	2	US-08-414-657D-43	Sequence 43, App1
179	116.5	6.9	338	4	US-09-135-080-4	Sequence 4, App1
180	116.5	6.9	607	2	US-08-752-307B-12	Sequence 12, App1
181	116.5	6.9	607	3	US-09-707-802-12	Sequence 12, App1
182	116.5	6.9	607	3	US-09-991-326-12	Sequence 12, App1
183	115.5	6.8	303	4	US-09-651-200-23	Sequence 23, App1
184	115.5	6.8	303	4	US-09-441-411-15	Sequence 15, App1
185	115.5	6.8	303	4	US-09-441-411-20	Sequence 20, App1
186	115.5	6.8	309	2	US-08-456-104-4	Sequence 4, App1
187	115.5	6.8	309	3	US-08-479-744A-23	Sequence 23, App1
188	115.5	6.8	309	3	US-08-800-757B-23	Sequence 23, App1
189	115.5	6.8	309	3	US-08-205-697A-21	Sequence 21, App1
190	115.5	6.8	309	3	US-08-702-525-21	Sequence 21, App1
191	115.5	6.8	309	4	US-09-651-200-22	Sequence 22, App1
192	115.5	6.8	309	4	US-09-667-135-33	Sequence 33, App1
193	115.5	6.8	309	4	US-09-425-762-23	Sequence 23, App1
194	115.5	6.8	309	4	US-09-837-867A-21	Sequence 21, App1
195	115.5	6.8	309	4	US-09-206-132-4	Sequence 4, App1
196	115.5	6.8	309	4	US-09-441-411-13	Sequence 13, App1
197	115.5	6.8	309	4	US-09-441-411-18	Sequence 18, App1
198	115.5	6.8	309	4	US-09-441-411-19	Sequence 19, App1
199	115.5	6.8	309	5	PCT-US95-02576-21	Sequence 21, App1
200	115.5	6.8	314	3	US-08-205-697A-13	Sequence 13, App1
201	115.5	6.8	314	3	US-08-702-525-13	Sequence 13, App1
202	115.5	6.8	314	4	US-09-837-867A-13	Sequence 13, App1
203	115.5	6.8	314	4	US-09-441-411-14	Sequence 14, App1
204	115.5	6.8	314	4	US-09-441-411-19	Sequence 19, App1
205	115.5	6.8	314	5	PCT-US95-02576-13	Sequence 13, App1
206	115.5	6.8	356	4	US-09-441-411-11	Sequence 11, App1
207	115.5	6.8	356	4	US-09-441-411-12	Sequence 12, App1
208	115.5	6.8	356	4	US-09-441-411-16	Sequence 16, App1
209	115.5	6.8	356	4	US-09-441-411-17	Sequence 17, App1
210	115.5	6.8	423	4	US-09-778-510-22	Sequence 22, App1
211	115.5	6.8	738	3	US-08-478-208-32	Sequence 32, App1
212	115.5	6.8	738	4	US-09-336-536-73	Sequence 73, App1
213	115.5	6.8	1253	3	US-08-506-296B-14	Sequence 14, App1
214	115	6.8	315	4	US-09-510-174B-28	Sequence 28, App1
215	115	6.8	315	4	US-09-620-461-28	Sequence 28, App1
216	115	6.8	1209	3	US-09-130-158A-2	Sequence 2, App1
217	114.5	6.8	431	3	US-09-038-832-2	Sequence 2, App1
218	114.5	6.8	431	3	US-09-038-832-4	Sequence 4, App1
219	114.5	6.8	479	4	US-09-723-368-2	Sequence 2, App1
220	113.5	6.7	624	4	US-08-467-602-326	Sequence 326, App
221	113.5	6.7	624	4	US-08-411-295F-252	Sequence 252, App
222	113.5	6.7	658	4	US-08-467-602-368	Sequence 368, App
223	113.5	6.7	658	4	US-08-411-295F-294	Sequence 294, App
224	113.5	6.7	841	4	US-08-467-602-337	Sequence 337, App
225	113.5	6.7	841	4	US-08-411-295F-253	Sequence 253, App
226	113.5	6.7	875	4	US-08-467-602-369	Sequence 369, App
227	113.5	6.7	875	4	US-08-411-295F-295	Sequence 295, App
228	113.5	6.7	888	4	US-08-467-602-325	Sequence 325, App
229	113.5	6.7	888	4	US-08-411-295F-251	Sequence 251, App
230	113.5	6.7	922	4	US-08-467-602-367	Sequence 367, App
231	113.5	6.7	922	4	US-08-411-295F-293	Sequence 293, App
232	113	6.7	287	2	US-08-414-657D-48	Sequence 48, App1
233	113	6.7	304	6	5260223-1	Patent No. 5260223
234	113	6.7	304	6	US-08-414-657D-44	Sequence 44, App1
235	113	6.7	497	4	US-09-499-846-6	Sequence 6, App1
236	113	6.7	497	4	US-09-499-846-10	Sequence 10, App1
237	112.5	6.7	517	4	US-09-723-368-4	Sequence 4, App1
238	112	6.6	287	2	US-08-414-657D-49	Sequence 49, App1
239	112	6.6	310	2	US-08-414-657D-45	Sequence 45, App1
240	112	6.6	322	3	US-09-383-586-33	Sequence 33, App1
241	112	6.6	322	4	US-09-823-038A-33	Sequence 33, App1
242	112	6.6	613	3	US-08-470-335-230	Sequence 230, App
243	112	6.6	613	4	US-08-467-602-329	Sequence 329, App
244	112	6.6	613	4	US-08-411-295F-255	Sequence 255, App
245	112	6.6	633	4	US-08-467-602-335	Sequence 335, App
246	112	6.6	633	4	US-08-411-295F-261	Sequence 261, App

247	112	6	6	647	4	US-08-467-602-371	Sequence 371, App	320	108	6	4	444	3	US-08-660-531-5	Sequence 5, Appl
248	112	6	6	647	4	US-08-411-295F-297	Sequence 297, App	321	108	6	4	868	1	US-08-374-834-1	Sequence 1, Appl
249	112	6	6	667	4	US-08-467-602-377	Sequence 377, App	322	108	6	4	868	2	US-08-644-277-1	Sequence 1, Appl
250	112	6	6	667	4	US-08-411-295F-303	Sequence 303, App	323	108	6	4	868	4	US-09-077-955-1	Sequence 1, Appl
251	112	6	6	830	3	US-08-470-335-231	Sequence 231, App	324	107.5	6	4	290	4	US-09-910-174B-19	Sequence 19, Appl
252	112	6	6	830	4	US-08-467-602-330	Sequence 330, App	325	107.5	6	4	290	4	US-09-620-461-1	Sequence 19, Appl
253	112	6	6	830	4	US-08-411-295F-256	Sequence 256, App	326	107.5	6	4	340	4	US-09-651-200-2	Sequence 2, Appl
254	112	6	6	830	4	US-08-467-602-336	Sequence 336, App	327	107.5	6	4	350	4	US-09-651-200-25	Sequence 25, Appl
255	112	6	6	850	4	US-08-411-295F-262	Sequence 262, App	328	107.5	6	4	350	4	US-09-910-174B-17	Sequence 17, Appl
256	112	6	6	864	4	US-08-467-602-372	Sequence 372, App	329	107.5	6	4	441	4	US-09-620-461-17	Sequence 17, Appl
257	112	6	6	864	4	US-08-411-295F-298	Sequence 298, App	330	107.5	6	4	450	4	US-09-651-200-4	Sequence 4, Appl
258	112	6	6	877	3	US-08-470-335-232	Sequence 232, App	331	107.5	6	4	1297	3	US-09-540-245A-17	Sequence 17, Appl
259	112	6	6	877	4	US-08-467-602-331	Sequence 331, App	332	107.5	6	4	1311	1	US-08-340-011-5	Sequence 5, Appl
260	112	6	6	877	4	US-08-411-295F-257	Sequence 257, App	333	107.5	6	4	1311	3	US-08-901-710-5	Sequence 5, Appl
261	112	6	6	884	4	US-08-467-602-378	Sequence 378, App	334	107	6	3	332	4	US-10-140-002-386	Sequence 386, App
262	112	6	6	884	4	US-08-411-295F-304	Sequence 304, App	335	107	6	3	624	2	US-08-642-406A-22	Sequence 22, App
263	112	6	6	897	4	US-08-467-602-337	Sequence 337, App	336	107	6	3	624	4	US-09-199-534-22	Sequence 22, App
264	112	6	6	897	4	US-08-411-295F-263	Sequence 263, App	337	107	6	3	624	4	US-09-199-534-22	Sequence 22, App
265	112	6	6	911	4	US-08-467-602-373	Sequence 373, App	338	107	6	3	733	3	US-08-434-000A-2	Sequence 2, Appl
266	112	6	6	911	4	US-08-411-295F-299	Sequence 299, App	339	107	6	3	733	3	US-09-312-157-2	Sequence 2, Appl
267	112	6	6	931	4	US-08-467-602-379	Sequence 379, App	340	106.5	6	3	731	1	US-07-921-807B-5	Sequence 5, Appl
268	112	6	6	931	4	US-08-411-295F-305	Sequence 305, App	341	106.5	6	3	731	1	US-08-441-944A-5	Sequence 5, Appl
269	112	6	6	946	5	PCT-US95-08493-13	Sequence 13, Appl	342	106.5	6	3	731	3	US-08-439-992A-3	Sequence 3, Appl
270	111.5	6	6	344	2	US-08-602-725-34	Sequence 34, Appl	343	106	6	3	729	1	US-07-640-029-3	Sequence 4, Appl
271	111	6	6	252	2	US-08-414-657D-56	Sequence 56, Appl	344	106	6	3	1474	4	US-09-677-046A-4	Sequence 4, Appl
272	111	6	6	252	2	US-08-414-657D-57	Sequence 57, Appl	345	106	6	3	1953	1	US-09-917-254-92	Sequence 92, Appl
273	110.5	6	5	349	4	US-09-924-103-1	Sequence 57, Appl	346	105.5	6	2	246	1	US-07-843-125-11	Sequence 11, Appl
274	110.5	6	5	330	2	US-08-979-424-4	Sequence 4, Appl	347	105.5	6	2	351	5	PCT-US93-05703-2	Sequence 2, Appl
275	110.5	6	5	330	4	US-09-907-794A-39	Sequence 39, Appl	348	105.5	6	2	408	3	US-09-724-864-62	Sequence 62, Appl
276	110.5	6	5	330	4	US-09-905-125A-39	Sequence 39, Appl	349	105.5	6	2	589	2	US-08-724-394A-1	Sequence 1, Appl
277	110.5	6	5	330	4	US-09-902-775A-39	Sequence 39, Appl	350	105.5	6	2	604	3	US-08-470-335-227	Sequence 27, App
278	110.5	6	5	330	4	US-09-906-700-39	Sequence 39, Appl	351	105.5	6	2	604	4	US-08-467-602-318	Sequence 318, App
279	110.5	6	5	330	4	US-10-140-002-338	Sequence 38, App	352	105.5	6	2	604	4	US-08-411-295F-244	Sequence 244, App
280	110.5	6	5	330	4	US-09-903-603A-39	Sequence 39, Appl	353	105.5	6	2	638	4	US-08-467-602-360	Sequence 360, App
281	110.5	6	5	513	4	US-09-910-174B-18	Sequence 18, Appl	354	105.5	6	2	638	4	US-08-411-295F-286	Sequence 286, App
282	110.5	6	5	513	4	US-09-620-461-18	Sequence 18, Appl	355	105.5	6	2	651	1	US-09-270-767-44877	Sequence 44877, A
283	110.5	6	5	518	4	US-09-919-172-30	Sequence 20, Appl	356	105.5	6	2	733	1	US-07-640-029-4	Sequence 4, Appl
284	110.5	6	5	1070	4	US-09-961-403-3	Sequence 3, Appl	357	105.5	6	2	733	1	US-07-921-807B-6	Sequence 6, Appl
285	110	6	5	316	4	US-09-910-174B-24	Sequence 24, Appl	358	105.5	6	2	733	1	US-08-441-944A-6	Sequence 6, Appl
286	110	6	5	316	4	US-09-620-461-24	Sequence 24, Appl	359	105.5	6	2	817	1	US-07-640-029-2	Sequence 2, Appl
287	110	6	5	547	1	US-08-314-615-1	Sequence 1, Appl	360	105.5	6	2	817	1	US-07-921-807B-3	Sequence 3, Appl
288	110	6	5	547	1	US-08-314-362-1	Sequence 1, Appl	361	105.5	6	2	820	1	US-08-439-992A-1	Sequence 1, Appl
289	110	6	5	547	1	US-08-433-010-1	Sequence 1, Appl	362	105.5	6	2	820	3	US-08-441-944A-3	Sequence 3, Appl
290	110	6	5	547	1	US-08-462-882-1	Sequence 1, Appl	363	105.5	6	2	820	3	US-08-439-992A-1	Sequence 1, Appl
291	110	6	5	547	2	US-08-483-389-1	Sequence 1, Appl	364	105.5	6	2	821	3	US-08-470-335-228	Sequence 28, App
292	110	6	5	547	2	US-08-487-113D-1	Sequence 1, Appl	365	105.5	6	2	821	4	US-08-467-602-319	Sequence 19, App
293	110	6	5	547	2	US-08-473-503-1	Sequence 1, Appl	366	105.5	6	2	821	4	US-08-411-295F-245	Sequence 245, App
294	110	6	5	547	2	US-08-483-932-1	Sequence 1, Appl	367	105.5	6	2	822	1	US-07-997-133B-1	Sequence 1, Appl
295	110	6	5	547	2	US-08-720-420A-1	Sequence 1, Appl	368	105.5	6	2	822	1	US-07-921-807B-4	Sequence 4, Appl
296	110	6	5	547	3	US-08-714-017-1	Sequence 1, Appl	369	105.5	6	2	822	1	US-08-459-296-2	Sequence 2, Appl
297	110	6	5	547	3	US-08-863-790-1	Sequence 1, Appl	370	105.5	6	2	822	1	US-08-441-944A-4	Sequence 4, Appl
298	110	6	5	547	3	US-08-475-680-1	Sequence 1, Appl	371	105.5	6	2	822	2	US-08-451-822A-12	Sequence 12, Appl
299	110	6	5	547	3	US-08-296-749-1	Sequence 1, Appl	372	105.5	6	2	822	3	US-08-439-992A-2	Sequence 2, Appl
300	110	6	5	917	1	US-08-245-395-2	Sequence 2, Appl	373	105.5	6	2	822	3	US-08-323-430-12	Sequence 12, Appl
301	110	6	5	917	1	US-08-481-130-2	Sequence 2, Appl	374	105.5	6	2	822	3	US-08-467-602-361	Sequence 361, App
302	110	6	5	917	1	US-08-656-984A-2	Sequence 2, Appl	375	105.5	6	2	825	4	US-08-411-295F-287	Sequence 287, App
303	110	6	5	917	1	US-08-485-604-2	Sequence 2, Appl	376	105.5	6	2	828	3	US-08-470-335-229	Sequence 229, App
304	110	6	5	917	2	US-08-487-595-2	Sequence 2, Appl	377	105.5	6	2	828	4	US-08-467-602-317	Sequence 317, App
305	110	6	5	477	4	US-10-140-002-50	Sequence 50, Appl	378	105.5	6	2	828	4	US-08-411-295F-243	Sequence 243, App
306	109.5	6	5	488	4	US-09-499-846-12	Sequence 12, Appl	379	105.5	6	2	829	1	US-08-374-834-16	Sequence 16, Appl
307	109.5	6	5	526	4	US-09-910-174B-9	Sequence 9, Appl	380	105.5	6	2	829	2	US-08-644-271-29	Sequence 29, Appl
308	109.5	6	5	526	4	US-09-620-461-9	Sequence 9, Appl	381	105.5	6	2	829	4	US-09-077-955-33	Sequence 33, Appl
309	109	6	5	339	4	US-09-719-243-2	Sequence 2, Appl	382	105.5	6	2	830	2	US-08-467-602-359	Sequence 359, App
310	109	6	5	358	4	US-09-719-243-3	Sequence 3, Appl	383	105.5	6	2	830	4	US-08-724-394A-4	Sequence 285, App
311	109	6	5	486	2	US-08-432-016-6	Sequence 6, Appl	384	105	6	2	830	2	US-08-261-304-2	Sequence 2, Appl
312	109	6	5	486	2	US-08-684-594-6	Sequence 6, Appl	385	105	6	2	830	4	US-09-677-046A-2	Sequence 412, App
313	109	6	5	525	4	US-09-499-846-4	Sequence 4, Appl	386	105	6	2	1509	4	US-09-976-594-531	Sequence 531, App
314	109	6	5	525	4	US-09-499-846-2	Sequence 2, Appl	387	104.5	6	2	1461	4	US-09-976-594-531	Sequence 531, App
315	109	6	5	622	4	US-09-499-846-8	Sequence 8, Appl	388	104.5	6	2	1461	4	US-09-976-594-531	Sequence 531, App
316	108.5	6	4	738	6	5264554-2	Patent No. 5264554	389	104	6	2	307	4	US-09-197-970B-3	Sequence 221, App
317	108	6	4	421	3	US-08-659-984A-1	Sequence 1, Appl	390	104	6	2	409	4	US-08-467-602-221	Sequence 147, App
318	108	6	4	421	3	US-08-660-531-1	Sequence 1, Appl	391	104	6	2	409	4	US-08-411-295F-147	Sequence 147, App
319	108	6	4	444	2	US-08-659-984A-5	Sequence 5, Appl	392	104	6	2	443	4	US-08-467-602-263	Sequence 263, App

393	104	6.2	443	4	US-08-411-295F-189	Sequence 189, App	466	102.5	6.1	696	4	US-08-467-602-268	Sequence 268, App
394	104	6.2	478	5	PCT-US95-08493-15	Sequence 15, App1	467	102.5	6.1	696	4	US-08-411-295F-194	Sequence 194, App
395	104	6.2	626	4	US-08-467-602-222	Sequence 222, App	468	102.5	6.1	701	4	US-08-467-602-356	Sequence 356, App
396	104	6.2	626	4	US-08-411-295F-148	Sequence 148, App	469	102.5	6.1	701	4	US-08-411-295F-282	Sequence 282, App
397	104	6.2	658	4	US-08-467-602-305	Sequence 305, App	470	102.5	6.1	716	4	US-08-467-602-274	Sequence 274, App
398	104	6.2	658	4	US-08-411-295F-231	Sequence 231, App	471	102.5	6.1	716	4	US-08-411-295F-200	Sequence 200, App
399	104	6.2	660	4	US-08-467-602-264	Sequence 264, App	472	102.5	6.1	864	3	US-08-470-335-244	Sequence 244, App
400	104	6.2	660	4	US-08-411-295F-190	Sequence 190, App	473	102.5	6.1	864	4	US-08-467-602-309	Sequence 309, App
401	104	6.2	673	4	US-08-467-602-220	Sequence 220, App	474	102.5	6.1	864	4	US-08-411-295F-235	Sequence 235, App
402	104	6.2	673	4	US-08-411-295F-146	Sequence 146, App	475	102.5	6.1	884	4	US-08-467-602-315	Sequence 315, App
403	104	6.2	632	4	US-08-467-602-347	Sequence 347, App	476	102.5	6.1	884	4	US-08-411-295F-241	Sequence 241, App
404	104	6.2	632	4	US-08-411-295F-273	Sequence 273, App	477	102.5	6.1	898	4	US-08-467-602-351	Sequence 351, App
405	104	6.2	707	4	US-08-467-602-262	Sequence 262, App	478	102.5	6.1	898	4	US-08-411-295F-277	Sequence 277, App
406	104	6.2	626	4	US-08-411-295F-188	Sequence 188, App	479	102.5	6.1	911	3	US-08-470-335-245	Sequence 245, App
407	104	6.2	860	5	PCT-US95-08493-19	Sequence 19, App1	480	102.5	6.1	911	4	US-08-467-602-310	Sequence 310, App
408	104	6.2	860	5	PCT-US95-08493-21	Sequence 21, App1	481	102.5	6.1	911	4	US-08-411-295F-236	Sequence 236, App
409	104	6.2	875	4	US-08-467-602-306	Sequence 306, App	482	102.5	6.1	918	4	US-08-467-602-357	Sequence 357, App
410	104	6.2	875	4	US-08-411-295F-232	Sequence 232, App	483	102.5	6.1	918	4	US-08-411-295F-283	Sequence 283, App
411	104	6.2	909	4	US-08-467-602-348	Sequence 348, App	484	102.5	6.1	931	4	US-08-467-602-316	Sequence 316, App
412	104	6.2	909	4	US-08-411-295F-274	Sequence 274, App	485	102.5	6.1	931	4	US-08-411-295F-242	Sequence 242, App
413	104	6.2	922	4	US-08-467-602-304	Sequence 304, App	486	102.5	6.1	945	4	US-08-467-602-352	Sequence 352, App
414	104	6.2	922	4	US-08-411-295F-220	Sequence 220, App	487	102.5	6.1	945	4	US-08-411-295F-278	Sequence 278, App
415	104	6.2	956	4	US-08-467-602-346	Sequence 346, App	488	102.5	6.1	965	4	US-08-467-602-358	Sequence 358, App
416	104	6.2	956	4	US-08-411-295F-272	Sequence 272, App	489	102.5	6.1	965	4	US-08-411-295F-284	Sequence 284, App
417	104	6.2	1503	4	US-09-677-046A-6	Sequence 6, App1	490	102.5	6.1	1184	2	US-08-918-914-1	Sequence 1, App1
418	103.5	6.1	534	4	US-09-651-200-6	Sequence 6, App1	491	102.5	6.1	1184	3	US-08-996-083-3	Sequence 3, App1
419	103.5	6.1	534	4	US-09-651-200-24	Sequence 24, App1	492	102	6.0	319	4	US-09-910-174B-12	Sequence 12, App1
420	103.5	6.1	668	1	US-08-232-538-13	Sequence 13, App1	493	102	6.0	319	4	US-09-620-461-12	Sequence 12, App1
421	103.5	6.1	668	2	US-08-786-164-13	Sequence 13, App1	494	102	6.0	347	4	US-09-667-174B-4	Sequence 4, App1
422	103.5	6.1	764	3	US-09-142-956B-14	Sequence 14, App1	495	102	6.0	357	4	US-09-910-174B-14	Sequence 14, App1
423	103.5	6.1	767	2	US-08-874-678-2	Sequence 2, App1	496	102	6.0	357	4	US-09-620-461-14	Sequence 14, App1
424	103.5	6.1	767	3	US-08-643-839-2	Sequence 2, App1	497	102	6.0	642	1	US-08-217-299-1	Sequence 1, App1
425	103.5	6.1	788	1	US-08-332-538-15	Sequence 2, App1	498	102	6.0	698	2	US-08-602-725-36	Sequence 36, App1
426	103.5	6.1	788	2	US-08-786-164-15	Sequence 15, App1	499	102	6.0	734	3	US-08-389-459A-17	Sequence 17, App1
427	103.5	6.1	1356	1	US-08-810-116-8	Sequence 8, App1	500	102	6.0	1439	3	US-08-987-867A-17	Sequence 17, App1
428	103.5	6.1	1356	2	US-07-930-548A-8	Sequence 8, App1	501	102	6.0	1260	4	US-09-134-000C-6133	Sequence 6133, App
429	103.5	6.1	1356	3	US-09-098-707A-2	Sequence 2, App1	502	101.5	6.0	318	6	US-09-506-296B-21	Sequence 21, App1
430	103.5	6.1	1356	3	US-09-483-539-2	Sequence 2, App1	503	101	6.0	318	6	5223394-11	Patent No. 5223394
431	103.5	6.1	1381	3	US-09-540-245A-16	Sequence 16, App1	504	101	6.0	394	4	US-08-466-368-2	Sequence 2, App1
432	103.5	6.1	1651	2	US-09-540-245A-18	Sequence 2, App1	505	101	6.0	394	4	US-08-328-500-2	Sequence 2, App1
433	103	6.1	240	2	US-07-956-399-2	Sequence 2, App1	506	101	6.0	458	3	US-09-517-605-3	Sequence 3, App1
434	103	6.1	806	3	US-09-383-630-3	Sequence 3, App1	507	101	6.0	801	3	US-09-383-630-6	Sequence 6, App1
435	102.5	6.1	326	5	US-08-225-477B-6	Sequence 6, App1	508	101	6.0	890	1	US-08-445-640-2	Sequence 2, App1
436	102.5	6.1	326	5	PCT-US95-04353-6	Sequence 6, App1	509	101	6.0	890	3	US-08-447-314-2	Sequence 2, App1
437	102.5	6.1	326	5	US-08-467-602-224	Sequence 224, App	510	101	6.0	890	3	US-08-445-461-2	Sequence 2, App1
438	102.5	6.1	398	4	US-08-411-295F-150	Sequence 150, App	511	101	6.0	911	1	US-08-286-305A-1	Sequence 1, App1
439	102.5	6.1	418	4	US-08-467-602-230	Sequence 230, App	512	101	6.0	911	2	US-08-441-104A-1	Sequence 1, App1
440	102.5	6.1	418	4	US-08-411-295F-156	Sequence 156, App	513	101	6.0	911	2	US-08-440-816A-1	Sequence 1, App1
441	102.5	6.1	432	4	US-08-467-602-266	Sequence 266, App	514	101	6.0	911	3	US-09-417-381A-1	Sequence 1, App1
442	102.5	6.1	432	4	US-08-411-295F-192	Sequence 192, App	515	101	6.0	304	3	US-08-862-124-14	Sequence 14, App1
443	102.5	6.1	452	4	US-08-467-602-272	Sequence 272, App	516	100.5	6.0	409	4	US-08-467-602-284	Sequence 284, App
444	102.5	6.1	452	4	US-08-411-295F-198	Sequence 198, App	517	100.5	6.0	409	4	US-08-411-295F-210	Sequence 210, App
445	102.5	6.1	458	4	US-09-435-956A-1	Sequence 1, App1	518	100.5	6.0	501	2	US-08-408-095-31	Sequence 31, App1
446	102.5	6.1	615	4	US-08-467-602-225	Sequence 225, App	519	100.5	6.0	626	4	US-08-467-602-285	Sequence 285, App
447	102.5	6.1	615	4	US-08-411-295F-151	Sequence 151, App	520	100.5	6.0	626	4	US-08-411-295F-211	Sequence 211, App
448	102.5	6.1	635	4	US-08-467-602-231	Sequence 231, App	521	100.5	6.0	638	3	US-08-470-335-240	Sequence 240, App
449	102.5	6.1	635	4	US-08-411-295F-157	Sequence 157, App	522	100.5	6.0	638	3	US-08-467-602-297	Sequence 297, App
450	102.5	6.1	647	3	US-08-470-335-243	Sequence 243, App	523	100.5	6.0	638	4	US-08-467-602-223	Sequence 223, App
451	102.5	6.1	647	3	US-08-411-295F-243	Sequence 243, App	524	100.5	6.0	638	4	US-08-411-295F-223	Sequence 223, App
452	102.5	6.1	647	4	US-08-467-602-308	Sequence 308, App	525	100.5	6.0	672	4	US-08-467-602-359	Sequence 359, App
453	102.5	6.1	647	4	US-08-411-295F-234	Sequence 234, App	526	100.5	6.0	672	4	US-08-411-295F-265	Sequence 265, App
454	102.5	6.1	649	4	US-08-467-602-267	Sequence 267, App	527	100.5	6.0	673	4	US-08-467-602-283	Sequence 283, App
455	102.5	6.1	649	4	US-08-411-295F-193	Sequence 193, App	528	100.5	6.0	673	4	US-08-411-295F-09	Sequence 09, App
456	102.5	6.1	662	4	US-08-467-602-225	Sequence 226, App	529	100.5	6.0	802	3	US-09-175-151A-33	Sequence 33, App1
457	102.5	6.1	662	4	US-08-411-295F-152	Sequence 152, App	530	100.5	6.0	855	3	US-08-470-335-241	Sequence 241, App
458	102.5	6.1	667	4	US-08-467-602-314	Sequence 314, App	531	100.5	6.0	855	3	US-08-467-602-298	Sequence 298, App
459	102.5	6.1	667	4	US-08-411-295F-240	Sequence 240, App	532	100.5	6.0	869	4	US-09-715-249-8	Sequence 8, App1
460	102.5	6.1	669	4	US-08-467-602-273	Sequence 273, App	533	100.5	6.0	889	4	US-08-411-295F-360	Sequence 360, App
461	102.5	6.1	669	4	US-08-411-295F-199	Sequence 199, App	534	100.5	6.0	889	4	US-08-467-602-330	Sequence 330, App
462	102.5	6.1	681	4	US-08-467-602-350	Sequence 350, App	535	100.5	6.0	889	4	US-08-411-295F-266	Sequence 266, App
463	102.5	6.1	681	4	US-08-411-295F-276	Sequence 276, App	536	100.5	6.0	902	3	US-08-470-335-242	Sequence 242, App
464	102.5	6.1	682	4	US-08-467-602-232	Sequence 232, App	537	100.5	6.0	902	4	US-08-467-602-296	Sequence 296, App
465	102.5	6.1	682	4	US-08-411-295F-158	Sequence 158, App	538	100.5	6.0	902	4	US-08-411-295F-222	Sequence 222, App

539	100.5	6.0	936	4	US-08-467-602-338	Sequence 338, App	612	98	5.8	874	2	US-08-456-647B-6	Sequence 6, App11
540	100.5	6.0	936	4	US-08-411-295F-264	Sequence 264, App	613	98	5.8	874	2	US-08-237-401A-6	Sequence 6, App11
541	100	5.9	63	4	US-09-397-243D-8	Sequence 8, App11	614	98	5.8	880	1	US-08-445-640-10	Sequence 10, App1
542	100	5.9	63	4	US-09-397-243D-10	Sequence 10, App1	615	98	5.8	880	3	US-08-170-558-10	Sequence 10, App1
543	100	5.9	134	4	US-09-858-664A-28	Sequence 28, App1	616	98	5.8	880	3	US-08-447-314-10	Sequence 10, App1
544	100	5.9	134	4	US-10-274-978-29	Sequence 29, App1	617	98	5.8	880	3	US-08-445-461-10	Sequence 10, App1
545	100	5.9	322	4	US-09-667-135-2	Sequence 2, App11	618	98	5.8	1021	1	US-08-497-025-3	Sequence 3, App11
546	100	5.9	322	4	US-09-910-174B-29	Sequence 29, App1	619	97.5	5.8	97	4	US-09-858-664A-27	Sequence 27, App1
547	100	5.9	322	4	US-09-620-461-29	Sequence 29, App1	620	97.5	5.8	97	4	US-10-574-978-28	Sequence 28, App1
548	100	5.9	448	4	US-10-092-138A-25	Sequence 25, App1	621	97.5	5.8	246	1	US-08-197-834-7	Sequence 7, App11
549	99.5	5.9	244	4	US-09-244-369B-1	Sequence 1, App11	622	97.5	5.8	342	2	US-08-724-394A-6	Sequence 6, App11
550	99.5	5.9	536	2	US-09-940-391-1	Sequence 1, App11	623	97.5	5.8	344	4	US-08-467-602-245	Sequence 245, App
551	99.5	5.9	536	2	US-08-752-307B-13	Sequence 13, App1	624	97.5	5.8	344	4	US-08-411-295F-171	Sequence 171, App
552	99.5	5.9	536	3	US-09-707-802-13	Sequence 13, App1	625	97.5	5.8	344	4	US-08-467-602-251	Sequence 251, App
553	99.5	5.9	536	3	US-09-991-326-13	Sequence 13, App1	626	97.5	5.8	344	4	US-08-411-295F-117	Sequence 171, App
554	99.5	5.9	610	3	US-08-470-335-836	Sequence 236, App	627	97.5	5.8	581	4	US-08-467-602-246	Sequence 246, App
555	99.5	5.9	610	4	US-08-467-602-332	Sequence 332, App	628	97.5	5.8	581	4	US-08-411-295F-112	Sequence 172, App
556	99.5	5.9	610	4	US-08-411-295F-258	Sequence 258, App	629	97.5	5.8	601	4	US-08-467-602-252	Sequence 252, App
557	99.5	5.9	644	4	US-08-467-602-374	Sequence 374, App	630	97.5	5.8	601	4	US-08-411-295F-118	Sequence 178, App
558	99.5	5.9	644	4	US-08-411-295F-300	Sequence 300, App	631	97.5	5.8	602	1	US-08-168-091A-2	Sequence 2, App1
559	99.5	5.9	827	3	US-08-470-335-237	Sequence 237, App	632	97.5	5.8	602	4	US-08-467-602-247	Sequence 247, App
560	99.5	5.9	827	4	US-08-467-602-333	Sequence 333, App	633	97.5	5.8	608	4	US-08-411-295F-113	Sequence 173, App
561	99.5	5.9	827	4	US-08-411-295F-259	Sequence 259, App	634	97.5	5.8	648	4	US-08-467-602-253	Sequence 253, App
562	99.5	5.9	861	4	US-08-467-602-375	Sequence 375, App	635	97.5	5.8	648	4	US-08-411-295F-119	Sequence 179, App
563	99.5	5.9	861	4	US-08-411-295F-301	Sequence 301, App	636	97.5	5.8	821	1	US-08-339-578-2	Sequence 2, App11
564	99.5	5.9	874	3	US-08-470-335-238	Sequence 238, App	637	97	5.7	340	3	US-09-188-930-184	Sequence 184, App
565	99.5	5.9	874	4	US-08-467-602-334	Sequence 334, App	638	97	5.7	340	4	US-09-312-283C-164	Sequence 184, App
566	99.5	5.9	874	4	US-08-411-295F-260	Sequence 260, App	639	97	5.7	338	2	US-08-284-391B-29	Sequence 29, App1
567	99.5	5.9	908	4	US-08-467-602-376	Sequence 376, App	640	97	5.7	338	3	US-09-218-950-29	Sequence 29, App1
568	99.5	5.9	908	4	US-08-411-295F-302	Sequence 302, App	641	97	5.7	338	4	US-08-394-388A-29	Sequence 29, App1
569	99	5.9	341	4	US-09-336-536-29	Sequence 29, App1	642	97	5.7	402	1	US-08-336-311-1	Sequence 1, App1
570	99	5.9	370	4	US-09-336-536-28	Sequence 28, App1	643	97	5.7	402	1	US-08-457-918-1	Sequence 1, App11
571	99	5.9	374	3	US-09-046-736-4	Sequence 4, App11	644	97	5.7	402	3	US-10-157-408-1	Sequence 1, App11
572	99	5.9	375	4	US-08-467-602-242	Sequence 242, App	645	97	5.7	457	4	US-08-328-500-9	Sequence 9, App11
573	99	5.9	375	4	US-08-411-295F-168	Sequence 168, App	646	97	5.7	458	3	US-08-466-368-4	Sequence 4, App11
574	99	5.9	388	1	US-08-445-640-6	Sequence 6, App11	647	97	5.7	462	2	US-08-417-495-5	Sequence 5, App11
575	99	5.9	388	3	US-08-170-558-6	Sequence 6, App11	648	97	5.7	462	2	US-08-384-391B-5	Sequence 5, App11
576	99	5.9	388	3	US-08-447-314-6	Sequence 6, App11	649	97	5.7	462	3	US-09-218-950-5	Sequence 5, App11
577	99	5.9	388	3	US-08-445-461-6	Sequence 6, App11	650	97	5.7	462	3	US-08-394-388A-5	Sequence 5, App11
578	99	5.9	394	6	5223418-2	Patent No. 5223418	651	97	5.7	462	5	PCT-US92-0178B-5	Sequence 5, App11
579	99	5.9	398	4	US-08-467-602-287	Sequence 287, App	652	97	5.7	532	2	PCT-US95-00454-5	Sequence 5, App11
580	99	5.9	398	4	US-08-411-295F-213	Sequence 213, App	653	97	5.7	532	2	PCT-US95-00454-6	Sequence 6, App11
581	99	5.9	418	4	US-08-467-602-293	Sequence 293, App	654	97	5.7	532	2	US-08-417-495-6	Sequence 6, App11
582	99	5.9	418	4	US-08-411-295F-219	Sequence 219, App	655	97	5.7	532	3	US-09-218-950-6	Sequence 6, App11
583	99	5.9	458	3	US-09-039-555B-15	Sequence 15, App1	656	97	5.7	532	4	US-08-394-388A-6	Sequence 6, App11
584	99	5.9	584	4	US-09-910-174B-16	Sequence 16, App1	657	97	5.7	532	5	PCT-US92-0178B-4	Sequence 6, App11
585	99	5.9	584	4	US-09-620-461-16	Sequence 16, App1	658	97	5.7	532	2	PCT-US95-00454-6	Sequence 6, App11
586	99	5.9	592	4	US-08-467-602-243	Sequence 243, App	659	97	5.7	535	2	US-08-417-495-4	Sequence 4, App11
587	99	5.9	592	4	US-08-411-295F-169	Sequence 169, App	660	97	5.7	535	2	US-08-384-391B-4	Sequence 4, App11
588	99	5.9	615	4	US-08-467-602-288	Sequence 288, App	661	97	5.7	535	3	US-09-218-950-4	Sequence 4, App11
589	99	5.9	615	4	US-08-411-295F-214	Sequence 214, App	662	97	5.7	535	4	US-08-394-388A-4	Sequence 4, App11
590	99	5.9	615	4	US-08-467-602-294	Sequence 294, App	663	97	5.7	535	5	PCT-US92-0178B-4	Sequence 4, App11
591	99	5.9	635	4	US-08-411-295F-220	Sequence 220, App	664	97	5.7	535	5	PCT-US95-00454-4	Sequence 4, App11
592	99	5.9	639	4	US-08-467-602-241	Sequence 241, App	665	97	5.7	601	3	US-08-470-335-233	Sequence 233, App
593	99	5.9	639	4	US-08-411-295F-167	Sequence 167, App	666	97	5.7	601	4	US-08-467-602-323	Sequence 233, App
594	99	5.9	662	4	US-08-467-602-289	Sequence 289, App	667	97	5.7	601	4	US-08-411-295F-249	Sequence 249, App
595	99	5.9	662	4	US-08-411-295F-215	Sequence 215, App	668	97	5.7	630	4	US-08-472-888A-6	Sequence 6, App11
596	99	5.9	662	4	US-08-467-602-295	Sequence 295, App	669	97	5.7	635	4	US-08-467-602-365	Sequence 365, App
597	99	5.9	682	4	US-08-411-295F-221	Sequence 221, App	670	97	5.7	635	4	US-08-411-295F-221	Sequence 221, App
598	98.5	5.8	324	4	US-09-910-174B-6	Sequence 6, App11	671	97	5.7	662	1	US-08-261-304-7	Sequence 7, App11
599	98.5	5.8	324	4	US-09-620-461-6	Sequence 6, App11	672	97	5.7	735	5	PCT-US93-00031-13	Sequence 13, App1
600	98.5	5.8	434	2	US-08-467-113D-120	Sequence 120, App	673	97	5.7	736	5	PCT-US93-00031-15	Sequence 15, App1
601	98.5	5.8	434	2	US-08-720-420A-120	Sequence 120, App	674	97	5.7	739	3	US-08-482-073-6	Sequence 6, App11
602	98.5	5.8	602	1	US-08-428-926-5	Sequence 5, App11	675	97	5.7	739	3	PCT-US93-00031-9	Sequence 9, App11
603	98.5	5.8	602	1	US-08-428-927-5	Sequence 5, App11	676	97	5.7	806	2	US-08-443-861-5	Sequence 5, App11
604	98.5	5.8	602	1	US-08-428-928-5	Sequence 5, App11	677	97	5.7	806	3	US-08-193-829B-5	Sequence 5, App11
605	98.5	5.8	602	1	US-08-428-928-5	Sequence 5, App11	678	97	5.7	818	3	US-08-470-335-234	Sequence 234, App
606	98.5	5.8	602	1	US-08-339-517-5	Sequence 5, App11	679	97	5.7	818	4	US-08-467-602-321	Sequence 321, App
607	98	5.8	240	4	US-09-270-767-321A	Sequence 321A, A	680	97	5.7	818	4	US-08-411-295F-247	Sequence 247, App
608	98	5.8	243	1	US-08-230-843-4	Sequence 4, App11	681	97	5.7	822	4	US-08-467-602-363	Sequence 363, App
609	98	5.8	243	2	US-08-636-936-4	Sequence 4, App11	682	97	5.7	852	4	US-08-411-295F-289	Sequence 289, App
610	98	5.8	246	4	US-09-336-536-31	Sequence 31, App1	683	97	5.7	865	3	US-08-470-335-235	Sequence 235, App
611	98	5.8	295	6	5223394-9	Patent No. 5223394	684	97	5.7	865	4	US-08-467-602-322	Sequence 322, App

685	97	5.7	865	4	US-08-411-295F-248	Sequence 248, App	758	95	5.6	649	4	US-09-269-939A-8	Sequence 8, App11
686	97	5.7	899	4	US-08-467-602-364	Sequence 364, App	759	95	5.6	879	1	US-08-554-461C-1	Sequence 1, App11
687	97	5.7	899	4	US-08-411-295F-230	Sequence 290, App	760	95	5.6	1501	2	US-08-447-464-3	Sequence 3, App11
688	97	5.7	1367	1	US-07-813-593-4	Sequence 4, App11	761	95	5.6	1501	2	US-08-716-679-3	Sequence 3, App11
689	97	5.7	1367	1	US-07-977-451-6	Sequence 6, App11	762	94.5	5.6	194	3	US-08-630-172-14	Sequence 14, App1
690	97	5.7	1367	1	US-07-946-507-4	Sequence 4, App11	763	94.5	5.6	194	3	US-09-375-418-14	Sequence 14, App1
691	97	5.7	1367	1	US-08-252-517-6	Sequence 6, App11	764	94.5	5.6	328	3	US-09-560-639-9	Sequence 9, App11
692	97	5.7	1367	1	US-07-906-397A-6	Sequence 6, App11	765	94.5	5.6	328	3	US-09-173-151A-25	Sequence 25, App1
693	97	5.7	1367	1	US-08-601-891-6	Sequence 6, App11	766	94.5	5.6	328	3	US-09-032-337-45	Sequence 45, App1
694	97	5.7	1367	2	US-08-443-861-2	Sequence 2, App11	767	94.5	5.6	477	2	US-08-359-705B-4	Sequence 4, App11
695	97	5.7	1367	2	US-09-021-324-6	Sequence 2, App11	768	94.5	5.6	477	2	US-08-286-846A-4	Sequence 4, App11
696	97	5.7	1367	3	US-08-193-829B-2	Sequence 6, App11	769	94.5	5.6	477	3	US-08-457-880A-4	Sequence 4, App11
697	97	5.7	1367	3	US-09-872-136B-6	Sequence 6, App11	770	94.5	5.6	477	3	US-08-444-622A-4	Sequence 4, App11
698	97	5.7	1367	5	PCT-US92-02750-8	Sequence 8, App11	771	94.5	5.6	477	3	US-08-942-562-4	Sequence 4, App11
699	97	5.7	1367	5	PCT-US92-05401-6	Sequence 6, App11	772	94.5	5.6	477	3	US-09-156-923-4	Sequence 4, App11
700	97	5.7	1367	5	PCT-US92-09893-6	Sequence 6, App11	773	94.5	5.6	556	3	US-09-560-639-8	Sequence 8, App11
701	96.5	5.7	158	3	US-09-560-639-13	Sequence 13, App1	774	94.5	5.6	610	2	US-08-724-394A-5	Sequence 5, App11
702	96.5	5.7	439	3	US-09-383-586-32	Sequence 32, App1	775	94.5	5.6	822	2	US-08-359-705B-2	Sequence 2, App11
703	96.5	5.7	439	4	US-09-823-038A-32	Sequence 32, App1	776	94.5	5.6	822	2	US-08-286-846A-2	Sequence 2, App11
704	96.5	5.7	489	4	US-09-667-135-30	Sequence 30, App1	777	94.5	5.6	822	2	US-08-457-880A-2	Sequence 2, App11
705	96.5	5.7	782	4	US-09-684-708A-21	Sequence 21, App1	778	94.5	5.6	822	3	US-08-444-622A-2	Sequence 2, App11
706	96.5	5.7	820	1	US-08-166-717D-6	Sequence 6, App1	779	94.5	5.6	822	3	US-08-942-562-2	Sequence 2, App11
707	96	5.7	389	4	US-08-467-602-213	Sequence 213, App	780	94.5	5.6	822	3	US-09-156-923-2	Sequence 2, App11
708	96	5.7	389	4	US-08-411-295F-129	Sequence 139, App	781	94.5	5.6	847	1	US-08-286-302A-5	Sequence 5, App11
709	96	5.7	423	4	US-08-467-602-255	Sequence 255, App	782	94.5	5.6	847	2	US-08-441-104A-5	Sequence 5, App11
710	96	5.7	423	4	US-08-467-602-255	Sequence 181, App	783	94.5	5.6	847	2	US-08-440-816A-5	Sequence 5, App11
711	96	5.7	469	3	US-08-753-007A-8	Sequence 8, App1	784	94.5	5.6	847	3	US-09-417-381A-5	Sequence 5, App11
712	96	5.7	469	3	US-09-398-496-8	Sequence 8, App1	785	94.5	5.6	888	1	US-08-445-640-35	Sequence 35, App1
713	96	5.7	606	4	US-08-467-602-214	Sequence 214, App	786	94.5	5.6	888	3	US-08-170-558-35	Sequence 35, App1
714	96	5.7	606	4	US-08-411-295F-140	Sequence 140, App	787	94.5	5.6	888	3	US-08-447-314-35	Sequence 35, App1
715	96	5.7	625	1	US-07-847-743B-26	Sequence 26, App1	788	94.5	5.6	888	3	US-08-445-461-35	Sequence 35, App1
716	96	5.7	625	1	US-08-456-201-26	Sequence 26, App1	789	94.5	5.6	910	4	US-09-313-942-28	Sequence 28, App1
717	96	5.7	625	2	US-08-456-241-26	Sequence 26, App1	790	94.5	5.6	999	4	US-08-252-626A-2	Sequence 2, App11
718	96	5.7	625	5	PCT-US92-04291A-26	Sequence 26, App1	791	94	5.6	198	4	US-09-569-611C-34	Sequence 34, App1
719	96	5.7	640	4	US-08-467-602-256	Sequence 256, App	792	94	5.6	203	4	US-09-270-761-60345	Sequence 60345, A
720	96	5.7	640	4	US-09-307-794A-292	Sequence 292, App	793	94	5.6	261	4	US-09-270-761-3898	Sequence 32898, A
721	96	5.7	640	4	US-09-905-125A-292	Sequence 292, App	794	94	5.6	261	4	US-09-270-761-48115	Sequence 48115, A
722	96	5.7	640	4	US-09-902-775A-292	Sequence 292, App	795	94	5.6	422	1	US-08-036-555B-170	Sequence 170, App
723	96	5.7	640	4	US-09-906-700-292	Sequence 292, App	796	94	5.6	422	1	US-08-469-565A-170	Sequence 170, App
724	96	5.7	640	4	US-10-140-002-368	Sequence 368, App	797	94	5.6	422	1	US-08-428-926-3	Sequence 3, App11
725	96	5.7	640	4	US-08-411-295F-182	Sequence 182, App	798	94	5.6	422	1	US-08-249-322A-170	Sequence 170, App
726	96	5.7	640	4	US-09-903-603A-292	Sequence 292, App	799	94	5.6	422	1	US-08-428-927-3	Sequence 3, App11
727	96	5.7	647	3	US-08-753-007A-32	Sequence 32, App1	800	94	5.6	422	1	US-08-428-298-3	Sequence 3, App11
728	96	5.7	647	3	US-09-398-496-32	Sequence 32, App1	801	94	5.6	422	1	US-08-339-517-3	Sequence 3, App11
729	96	5.7	650	3	US-09-310-463-2	Sequence 2, App11	802	94	5.6	422	1	US-08-469-526A-170	Sequence 170, App
730	96	5.7	650	4	US-08-842-248A-2	Sequence 2, App11	803	94	5.6	422	2	US-08-734-591A-170	Sequence 170, App
731	96	5.7	651	3	US-08-985-950-22	Sequence 22, App1	804	94	5.6	422	2	US-08-469-660-170	Sequence 170, App
732	96	5.7	651	4	US-09-546-049-22	Sequence 22, App1	805	94	5.6	422	3	US-08-341-018-72	Sequence 72, App1
733	96	5.7	653	4	US-08-467-602-212	Sequence 212, App	806	94	5.6	422	3	US-08-470-335-170	Sequence 170, App
734	96	5.7	653	4	US-08-411-295F-118	Sequence 138, App	807	94	5.6	422	3	US-08-735-021-170	Sequence 170, App
735	96	5.7	669	1	US-07-847-743B-8	Sequence 8, App1	808	94	5.6	422	3	US-08-734-664A-170	Sequence 170, App
736	96	5.7	669	1	US-07-847-743B-13	Sequence 13, App1	809	94	5.6	422	3	US-08-470-339-170	Sequence 170, App
737	96	5.7	669	1	US-08-456-201-8	Sequence 8, App1	810	94	5.6	422	4	US-08-467-603-170	Sequence 170, App
738	96	5.7	669	1	US-08-456-201-13	Sequence 13, App1	811	94	5.6	422	4	US-08-411-295F-65	Sequence 65, App1
739	96	5.7	669	2	US-08-330-161-11	Sequence 11, App1	812	94	5.6	422	4	US-08-411-295F-66	Sequence 66, App1
740	96	5.7	669	2	US-08-456-241-8	Sequence 8, App11	813	94	5.6	422	4	US-08-411-295F-69	Sequence 69, App1
741	96	5.7	669	2	US-08-456-241-13	Sequence 13, App1	814	94	5.6	422	4	US-08-411-295F-103	Sequence 103, App
742	96	5.7	669	2	US-08-440-401-11	Sequence 11, App1	815	94	5.6	422	5	PCT-US94-05083C-166	Sequence 166, App
743	96	5.7	669	2	US-08-419-878B-11	Sequence 11, App1	816	94	5.6	422	5	PCT-US94-05083C-185	Sequence 185, App
744	96	5.7	669	3	US-09-173-480-11	Sequence 11, App1	817	94	5.6	422	5	PCT-US95-06846A-170	Sequence 170, App
745	96	5.7	669	3	PCT-US92-04295A-8	Sequence 8, App11	818	94	5.6	458	6	5223394-7	Patent No. 5223394
746	96	5.7	669	5	PCT-US92-04295A-13	Sequence 254, App	819	94	5.6	635	4	US-08-467-602-302	Sequence 302, App
747	96	5.7	687	4	US-08-467-602-254	Sequence 180, App	820	94	5.6	635	4	US-08-411-295F-228	Sequence 228, App
748	96	5.7	687	4	US-08-411-295F-180	Sequence 8, App11	821	94	5.6	635	4	US-09-569-611C-35	Sequence 35, App1
749	96	5.7	1140	4	US-09-579-692B-8	Sequence 258, App	822	94	5.6	635	4	US-08-467-602-344	Sequence 270, App
750	96	5.7	1638	4	US-09-071-035-258	Sequence 262, App	823	94	5.6	669	4	US-08-411-295F-470	Sequence 34, App1
751	96	5.7	1638	4	US-09-071-035-262	Sequence 266, App	824	94	5.6	805	3	US-08-985-526-34	Sequence 34, App1
752	96	5.7	1747	4	US-09-071-035-266	Sequence 5999, App	825	94	5.6	852	3	US-08-470-335-248	Sequence 248, App
753	96	5.7	1747	4	US-09-134-000C-5599	Sequence 4, App1	826	94	5.6	852	4	US-08-467-602-300	Sequence 300, App
754	95.5	5.7	652	3	US-09-310-463-4	Sequence 4, App11	827	94	5.6	852	4	US-08-411-295F-326	Sequence 326, App
755	95.5	5.7	652	3	US-08-842-248A-4	Sequence 17, App1	828	94	5.6	886	4	US-08-467-602-342	Sequence 342, App
756	95	5.6	287	3	US-08-862-124-17	Sequence 14, App1	829	94	5.6	886	4	US-08-411-295F-468	Sequence 268, App
757	95	5.6	649	4	US-09-499-522-14		830	94	5.6	886	4		

831	94	5.6	899	3	US-08-470-335-249	Sequence 249, App	904	92	5.5	302	4	US-09-549-067A-32	Sequence 32, App1
832	94	5.6	899	4	US-08-467-602-301	Sequence 301, App	905	92	5.5	351	4	US-09-756-983-18	Sequence 18, App1
833	94	5.6	899	4	US-08-411-295F-227	Sequence 227, App	906	92	5.5	411	3	US-08-470-339-189	Sequence 189, App
834	94	5.6	933	4	US-08-467-602-343	Sequence 343, App	907	92	5.5	414	3	US-08-470-339-188	Sequence 188, App
835	94	5.6	933	4	US-08-411-295F-269	Sequence 269, App	908	92	5.5	422	3	US-08-753-007A-9	Sequence 9, App1
836	94	5.6	983	3	US-09-412-554A-2	Sequence 2, App1	909	92	5.5	422	3	US-09-398-496-9	Sequence 9, App1
837	93.5	5.5	143	2	US-08-653-402B-8	Sequence 8, App1	910	92	5.5	422	4	US-08-467-602-234	Sequence 324, App
838	93.5	5.5	259	3	US-09-560-639-11	Sequence 11, App1	911	92	5.5	422	4	US-08-411-295F-225	Sequence 225, App
839	93.5	5.5	296	4	US-09-667-135-36	Sequence 36, App1	912	92	5.5	425	3	US-08-470-335-226	Sequence 226, App
840	93.5	5.5	323	4	US-09-651-200-21	Sequence 21, App1	913	92	5.5	425	4	US-08-467-602-320	Sequence 320, App
841	93.5	5.5	323	4	US-09-441-411-22	Sequence 22, App1	914	92	5.5	425	4	US-08-411-295F-246	Sequence 246, App
842	93.5	5.5	323	5	PCT-US94-09642-2	Sequence 2, App1	915	92	5.5	456	3	US-08-470-335-246	Sequence 246, App
843	93.5	5.5	329	2	US-08-456-104-2	Sequence 2, App1	916	92	5.5	456	4	US-08-467-602-303	Sequence 303, App
844	93.5	5.5	329	2	US-08-101-624-2	Sequence 2, App1	917	92	5.5	456	4	US-08-467-602-166	Sequence 166, App
845	93.5	5.5	329	3	US-08-479-744A-2	Sequence 2, App1	918	92	5.5	456	4	US-08-411-295F-229	Sequence 229, App
846	93.5	5.5	329	3	US-08-280-757B-2	Sequence 2, App1	919	92	5.5	456	4	US-08-411-295F-292	Sequence 292, App
847	93.5	5.5	329	3	US-08-205-697A-23	Sequence 23, App1	920	92	5.5	459	3	US-08-470-335-239	Sequence 239, App
848	93.5	5.5	329	3	US-08-702-525-23	Sequence 23, App1	921	92	5.5	459	4	US-08-467-602-299	Sequence 299, App
849	93.5	5.5	329	3	US-08-403-253A-4	Sequence 4, App1	922	92	5.5	459	4	US-08-467-602-162	Sequence 162, App
850	93.5	5.5	329	4	US-08-435-816A-4	Sequence 4, App1	923	92	5.5	459	4	US-08-411-295F-225	Sequence 225, App
851	93.5	5.5	329	4	US-09-425-762-2	Sequence 2, App1	924	92	5.5	459	4	US-08-411-295F-288	Sequence 288, App
852	93.5	5.5	329	4	US-09-837-867A-23	Sequence 23, App1	925	92	5.5	479	4	US-08-467-602-307	Sequence 307, App
853	93.5	5.5	329	4	US-09-206-132-2	Sequence 2, App1	926	92	5.5	479	4	US-08-411-295F-233	Sequence 233, App
854	93.5	5.5	329	4	US-09-441-411-26	Sequence 26, App1	927	92	5.5	490	4	US-08-467-602-245	Sequence 245, App
855	93.5	5.5	329	5	PCT-US95-02576-23	Sequence 23, App1	928	92	5.5	490	4	US-08-411-295F-271	Sequence 271, App
856	93.5	5.5	388	1	US-08-445-640-12	Sequence 12, App1	929	92	5.5	493	4	US-08-467-602-241	Sequence 241, App
857	93.5	5.5	388	3	US-08-170-558-12	Sequence 12, App1	930	92	5.5	493	4	US-08-411-295F-267	Sequence 267, App
858	93.5	5.5	388	3	US-08-447-314-12	Sequence 12, App1	931	92	5.5	513	4	US-08-467-602-349	Sequence 349, App
859	93.5	5.5	388	3	US-08-445-461-12	Sequence 12, App1	932	92	5.5	513	4	US-08-411-295F-275	Sequence 275, App
860	93.5	5.5	434	1	US-08-236-311-4	Sequence 4, App1	933	92	5.5	613	4	US-08-800-729-82	Sequence 82, App1
861	93.5	5.5	434	3	US-08-457-918-4	Sequence 4, App1	934	92	5.5	613	4	US-08-470-335-250	Sequence 250, App
862	93.5	5.5	445	4	US-10-157-408-4	Sequence 4, App1	935	92	5.5	644	3	US-08-800-729-88	Sequence 88, App
863	93.5	5.5	445	4	US-08-467-602-328	Sequence 328, App	936	92	5.5	644	4	US-08-467-602-311	Sequence 311, App
864	93.5	5.5	445	4	US-08-411-295F-254	Sequence 254, App	937	92	5.5	644	4	US-08-411-295F-237	Sequence 237, App
865	93.5	5.5	479	4	US-08-467-602-370	Sequence 370, App	938	92	5.5	678	4	US-08-467-602-353	Sequence 353, App
866	93.5	5.5	479	4	US-08-411-295F-296	Sequence 296, App	939	92	5.5	678	4	US-08-411-295F-279	Sequence 279, App
867	93.5	5.5	770	1	US-08-525-654A-3	Sequence 1, App1	940	92	5.5	861	3	US-08-470-335-251	Sequence 251, App
868	93.5	5.5	771	1	US-08-525-654A-3	Sequence 1, App1	941	92	5.5	861	4	US-08-467-602-212	Sequence 212, App
869	93	5.5	309	4	US-09-667-135-6	Sequence 3, App1	942	92	5.5	861	4	US-08-411-295F-238	Sequence 238, App
870	93	5.5	309	4	US-09-910-174B-7	Sequence 6, App1	943	92	5.5	895	4	US-08-467-602-354	Sequence 354, App
871	93	5.5	309	4	US-09-620-461-7	Sequence 7, App1	944	92	5.5	895	4	US-08-411-295F-280	Sequence 280, App
872	93	5.5	523	4	US-09-910-174B-11	Sequence 11, App1	945	92	5.5	908	3	US-08-470-335-252	Sequence 252, App
873	93	5.5	523	4	US-09-620-461-11	Sequence 11, App1	946	92	5.5	908	4	US-08-467-602-113	Sequence 113, App
874	93	5.5	558	4	US-09-667-135-31	Sequence 31, App1	947	92	5.5	908	4	US-08-411-295F-239	Sequence 239, App
875	93	5.5	581	2	US-08-724-394A-3	Sequence 3, App1	948	92	5.5	942	4	US-08-467-602-355	Sequence 355, App
876	92.5	5.5	282	4	US-09-404-879A-393	Sequence 393, App	949	92	5.5	942	4	US-08-411-295F-281	Sequence 281, App
877	92.5	5.5	282	4	US-09-667-857-393	Sequence 393, App	950	92	5.5	287	4	US-09-318-786-17	Sequence 17, App1
878	92.5	5.5	309	4	US-09-404-879A-392	Sequence 392, App	951	91.5	5.4	338	1	US-08-442-043A-17	Sequence 17, App1
879	92.5	5.5	309	4	US-09-667-857-392	Sequence 392, App	952	91.5	5.4	338	4	US-08-441-893A-17	Sequence 17, App1
880	92.5	5.5	329	4	US-09-667-135-32	Sequence 32, App1	953	91.5	5.4	388	3	US-09-108-930-275	Sequence 275, App
881	92.5	5.5	389	4	US-08-467-602-276	Sequence 276, App	954	92	5.4	388	4	US-09-312-893C-275	Sequence 275, App
882	92.5	5.5	389	4	US-08-411-295F-202	Sequence 202, App	955	91.5	5.4	576	1	US-07-821-716-4	Sequence 4, App1
883	92.5	5.5	424	6	5169835-6	Patent No. 5169835	956	91.5	5.4	576	2	US-08-381-603-4	Sequence 4, App1
884	92.5	5.5	426	1	US-08-336-583-2	Sequence 2, App1	957	91.5	5.4	576	3	US-08-924-376-4	Sequence 4, App1
885	92.5	5.5	426	5	PCT-US95-13795-2	Sequence 2, App1	958	91.5	5.4	576	3	US-08-685-112-4	Sequence 4, App1
886	92.5	5.5	606	4	US-08-467-602-277	Sequence 277, App	959	91.5	5.4	576	3	US-09-173-151A-30	Sequence 30, App1
887	92.5	5.5	606	4	US-08-411-295F-203	Sequence 203, App	960	91.5	5.4	576	3	US-08-466-932A-4	Sequence 4, App1
888	92.5	5.5	608	3	US-09-095-385-4	Sequence 4, App1	961	91.5	5.4	576	5	PCT-US94-02414-4	Sequence 4, App1
889	92.5	5.5	653	4	US-08-467-602-275	Sequence 275, App	962	91.5	5.4	576	5	PCT-US96-08899-4	Sequence 4, App1
890	92.5	5.5	653	4	US-08-411-295F-201	Sequence 201, App	963	91.5	5.4	643	5	PCT-US93-00031-19	Sequence 19, App1
891	92.5	5.5	746	3	US-08-434-000A-4	Sequence 4, App1	964	91.5	5.4	644	5	PCT-US93-00031-21	Sequence 21, App1
892	92.5	5.5	746	3	US-09-312-157-4	Sequence 4, App1	965	91.5	5.4	647	3	US-09-009-490A-91	Sequence 91, App1
893	92.5	5.5	887	4	US-09-340-236-9911	Sequence 2911, App	966	91.5	5.4	647	3	US-08-482-073-5	Sequence 91, App1
894	92	5.5	95	3	US-08-928-383B-17	Sequence 17, App1	967	91.5	5.4	647	5	PCT-US93-00031-11	Sequence 11, App1
895	92	5.5	274	4	US-09-813-659-30	Sequence 30, App1	968	91.5	5.4	647	5	PCT-US93-00031-17	Sequence 17, App1
896	92	5.5	274	4	US-09-549-067A-30	Sequence 30, App1	969	91.5	5.4	740	5	PCT-US93-00031-13	Sequence 13, App1
897	92	5.5	302	1	US-08-121-054C-18	Sequence 18, App1	970	91.5	5.4	1241	3	US-09-040-774-2	Sequence 2, App1
898	92	5.5	302	1	US-08-121-054C-30	Sequence 30, App1	971	91.5	5.4	1911	1	US-08-348-006B-5	Sequence 5, App1
899	92	5.5	302	3	US-08-538-436-18	Sequence 18, App1	972	91.5	5.4	1911	2	US-08-800-825A-5	Sequence 5, App1
900	92	5.5	302	3	US-08-538-436-18	Sequence 18, App1	973	91.5	5.4	1911	3	US-09-158-657-5	Sequence 5, App1
901	92	5.5	302	4	US-09-813-659-18	Sequence 18, App1	974	91.5	5.4	1911	5	PCT-US94-10166-5	Sequence 5, App1
902	92	5.5	302	4	US-09-813-659-32	Sequence 32, App1	975	91	5.4	355	4	US-08-467-602-234	Sequence 234, App
903	92	5.5	302	4	US-09-549-067A-18	Sequence 18, App1	976	91	5.4	355	4	US-08-411-295F-160	Sequence 160, App

977	91	5.4	371	4	US-08-411-295F-308	Sequence 308, App	1050	89	5.3	583	2	US-08-432-016-2	Sequence 2, App1
978	91	5.4	405	4	US-08-467-602-384	Sequence 384, App	1051	89	5.3	583	1	US-08-684-594-2	Sequence 2, App1
979	91	5.4	405	4	US-08-411-295F-307	Sequence 307, App	1052	89	5.3	643	1	US-08-471-570-6	Sequence 6, App1
980	91	5.4	477	2	US-08-432-016-3	Sequence 3, App1	1053	89	5.3	769	1	US-08-471-570-8	Sequence 8, App1
981	91	5.4	477	2	US-08-684-594-3	Sequence 4, App1	1054	88.5	5.2	112	2	US-08-454-236-3	Sequence 3, App1
982	91	5.4	556	1	US-08-471-570-4	Sequence 255, App	1055	88.5	5.2	135	2	US-08-454-236-2	Sequence 2, App1
983	91	5.4	572	4	US-08-467-602-235	Sequence 255, App	1056	88.5	5.2	252	4	US-09-370-767-44627	Sequence 4627, A
984	91	5.4	572	4	US-08-411-295F-161	Sequence 161, App	1057	88.5	5.2	622	2	US-08-356-786-16	Sequence 16, App1
985	91	5.4	581	4	US-09-499-522-18	Sequence 12, App1	1058	88	5.2	181	3	US-08-753-007A-4	Sequence 4, App1
986	91	5.4	581	4	US-09-269-939A-12	Sequence 233, App	1059	88	5.2	181	3	US-09-398-496-4	Sequence 4, App1
987	91	5.4	619	4	US-08-467-602-233	Sequence 159, App	1060	88	5.2	224	4	US-09-530-139-38	Sequence 38, App1
988	91	5.4	619	4	US-08-411-295F-159	Sequence 159, App	1061	88	5.2	317	4	US-09-684-708A-23	Sequence 23, App1
989	91	5.4	652	1	US-08-471-570-10	Sequence 11, App1	1062	88	5.2	407	3	US-08-753-007A-6	Sequence 6, App1
990	91	5.4	816	1	US-07-640-029-1	Sequence 11, App1	1063	88	5.2	407	3	US-09-398-496-6	Sequence 6, App1
991	91	5.4	76	4	US-09-397-243D-11	Sequence 6, App1	1064	88	5.2	421	4	US-09-569-611C-35	Sequence 36, App1
992	90.5	5.4	310	3	US-08-477-660B-6	Sequence 6, App1	1065	88	5.2	490	4	US-09-963-137-199	Sequence 199, App
993	90.5	5.4	310	3	US-08-379-516-6	Sequence 6, App1	1066	88	5.2	605	2	US-08-752-307B-8	Sequence 8, App1
994	90.5	5.4	310	3	US-09-329-916-6	Sequence 6, App1	1067	88	5.2	605	2	US-08-753-007A-2	Sequence 2, App1
995	90.5	5.4	310	3	US-08-485-372A-6	Sequence 6, App1	1068	88	5.2	605	3	US-09-398-496-2	Sequence 2, App1
996	90.5	5.4	310	3	US-09-409-006A-6	Sequence 6, App1	1069	88	5.2	605	3	US-09-707-802-8	Sequence 8, App1
997	90.5	5.4	310	4	US-08-484-681-6	Sequence 6, App1	1070	88	5.2	605	3	US-09-991-326-8	Sequence 8, App1
998	90.5	5.4	310	4	US-09-766-995-6	Sequence 6, App1	1071	88	5.2	731	4	US-09-910-174B-15	Sequence 15, App1
999	90.5	5.4	310	5	PCT-US93-07422-6	Sequence 6, App1	1072	88	5.2	731	4	US-09-620-461-15	Sequence 15, App1
1000	90.5	5.4	330	2	US-08-525-864A-4	Sequence 4, App1	1073	88	5.2	1183	4	US-09-532-310B-5	Sequence 5, App1
1001	90.5	5.4	433	3	US-09-100-409A-1	Sequence 1, App1	1074	87.5	5.2	205	1	US-07-870-029-2	Sequence 2, App1
1002	90.5	5.4	754	2	US-08-525-864A-2	Sequence 2, App1	1075	87.5	5.2	205	1	US-08-233-005-2	Sequence 2, App1
1003	90	5.3	170	4	US-09-270-767-43106	Sequence 43106, A	1076	87.5	5.2	205	1	US-08-428-943-2	Sequence 2, App1
1004	90	5.3	240	2	US-08-800-198-8	Sequence 8, App1	1077	87.5	5.2	205	3	US-09-016-649-2	Sequence 2, App1
1005	90	5.3	240	3	US-09-296-595-8	Sequence 8, App1	1078	87.5	5.2	205	5	PCT-US95-0485B-2	Sequence 2, App1
1006	90	5.3	288	4	US-09-651-200-14	Sequence 14, App1	1079	87.5	5.2	386	4	US-08-467-602-218	Sequence 218, App
1007	90	5.3	230	4	US-09-910-174B-32	Sequence 32, App1	1080	87.5	5.2	420	1	US-08-411-295F-144	Sequence 144, App
1008	90	5.3	395	4	US-08-467-602-227	Sequence 227, App	1081	87.5	5.2	420	1	US-07-847-743B-29	Sequence 29, App1
1009	90	5.3	395	4	US-08-411-295F-153	Sequence 153, App	1082	87.5	5.2	420	1	US-08-456-201-29	Sequence 29, App1
1010	90	5.3	429	4	US-08-467-602-269	Sequence 269, App	1083	87.5	5.2	420	2	US-08-456-241-29	Sequence 29, App1
1011	90	5.3	429	4	US-08-411-295F-195	Sequence 195, App	1084	87.5	5.2	420	4	US-08-467-602-260	Sequence 260, App
1012	90	5.3	433	2	US-08-867-149-1	Sequence 1, App1	1085	87.5	5.2	420	4	US-08-411-295F-186	Sequence 186, App1
1013	90	5.3	433	2	US-08-808-374-1	Sequence 1, App1	1086	87.5	5.2	420	5	PCT-US92-04295A-29	Sequence 29, App1
1014	90	5.3	444	3	US-09-540-245A-19	Sequence 19, App1	1087	87.5	5.2	473	3	US-09-828-995B-20	Sequence 20, App1
1015	90	5.3	553	2	US-08-661-052-16	Sequence 16, App1	1088	87.5	5.2	603	4	US-08-467-602-216	Sequence 216, App
1016	90	5.3	553	3	US-09-188-082-16	Sequence 16, App1	1089	87.5	5.2	603	4	US-08-411-295F-142	Sequence 142, App
1017	90	5.3	553	3	US-09-364-088-16	Sequence 16, App1	1090	87.5	5.2	637	1	US-07-847-743B-28	Sequence 28, App1
1018	90	5.3	553	3	US-09-102-716-16	Sequence 16, App1	1091	87.5	5.2	637	2	US-08-456-201-28	Sequence 28, App1
1019	90	5.3	582	4	US-09-702-705-334	Sequence 334, App	1092	87.5	5.2	637	2	US-08-456-241-28	Sequence 28, App1
1020	90	5.3	582	4	US-09-736-457-334	Sequence 334, App	1093	87.5	5.2	637	4	US-08-467-602-258	Sequence 258, App
1021	90	5.3	582	4	US-09-614-124B-334	Sequence 334, App	1094	87.5	5.2	637	4	US-08-411-295F-184	Sequence 184, App
1022	90	5.3	582	4	US-09-671-325-334	Sequence 334, App	1095	87.5	5.2	637	5	PCT-US92-04295A-28	Sequence 28, App1
1023	90	5.3	582	4	US-09-589-184-334	Sequence 334, App	1096	87.5	5.2	637	4	US-08-467-602-217	Sequence 217, App
1024	90	5.3	582	4	US-09-658-824-334	Sequence 334, App	1097	87.5	5.2	650	4	US-08-411-295F-143	Sequence 143, App
1025	90	5.3	593	4	US-09-269-939A-2	Sequence 2, App1	1098	87.5	5.2	684	4	US-08-467-602-259	Sequence 259, App
1026	90	5.3	612	4	US-08-467-602-228	Sequence 228, App	1099	87.5	5.2	684	4	US-08-411-295F-185	Sequence 185, App
1027	90	5.3	612	4	US-08-411-295F-154	Sequence 154, App	1100	87.5	5.2	698	4	US-09-579-692B-60	Sequence 60, App1
1028	90	5.3	646	4	US-08-467-602-270	Sequence 270, App	1101	87	5.2	349	3	US-08-470-335-188	Sequence 188, App
1029	90	5.3	646	4	US-08-471-295F-196	Sequence 196, App	1102	87	5.2	364	4	US-08-896-537A-3	Sequence 3, App1
1030	90	5.3	659	4	US-08-467-602-229	Sequence 229, App	1103	87	5.2	382	4	US-08-697-602-382	Sequence 382, App1
1031	90	5.3	659	4	US-08-411-295F-155	Sequence 155, App	1104	87	5.2	653	4	US-09-520-781-1	Sequence 10, App1
1032	90	5.3	693	4	US-08-467-602-271	Sequence 271, App	1105	87	5.2	653	4	US-10-140-002-438	Sequence 438, App
1033	90	5.3	693	4	US-08-411-295F-197	Sequence 197, App	1106	87	5.2	666	3	US-09-423-439-51	Sequence 51, App1
1034	90	5.3	821	2	US-08-451-822A-13	Sequence 13, App1	1107	87	5.2	668	3	US-09-173-151A-35	Sequence 35, App1
1035	90	5.3	821	3	US-08-323-430-13	Sequence 13, App1	1108	87	5.2	771	3	US-08-434-000A-8	Sequence 8, App1
1036	90	5.3	1018	1	US-08-408-093-6	Sequence 6, App1	1109	87	5.2	771	3	US-09-312-157-8	Sequence 8, App1
1037	90	5.3	1018	1	US-08-408-420A-6	Sequence 6, App1	1110	86.5	5.1	90	2	US-08-454-236-4	Sequence 4, App1
1038	90	5.3	1018	1	US-08-714-901-6	Sequence 6, App1	1111	86.5	5.1	218	5	PCT-US94-14106-57	Sequence 57, App1
1039	90	5.3	1018	3	US-08-040-741-6	Sequence 6, App1	1112	86.5	5.1	230	3	US-09-485-737B-102	Sequence 102, App
1040	89.5	5.3	1170	4	US-09-260-527-1	Sequence 1, App1	1113	86.5	5.1	395	4	US-08-467-602-290	Sequence 290, App
1041	89.5	5.3	1170	4	US-09-749-588-2	Sequence 2, App1	1114	86.5	5.1	395	4	US-08-411-295F-216	Sequence 216, App
1042	89.5	5.3	93	3	US-08-928-383B-19	Sequence 19, App1	1115	86.5	5.1	612	4	US-08-467-602-291	Sequence 291, App
1043	89	5.3	287	4	US-09-800-729-114	Sequence 114, App1	1116	86.5	5.1	659	4	US-08-411-295F-217	Sequence 217, App
1044	89	5.3	287	4	US-09-800-729-153	Sequence 153, App	1117	86.5	5.1	659	4	US-08-467-602-292	Sequence 292, App
1045	89	5.3	297	4	US-09-486-814A-2	Sequence 2, App1	1118	86.5	5.1	659	4	US-08-411-295F-218	Sequence 218, App
1046	89	5.3	327	4	US-09-684-708A-27	Sequence 27, App1	1119	86.5	5.1	826	4	US-09-071-035-264	Sequence 264, App
1047	89	5.3	327	4	US-09-684-708A-27	Sequence 27, App1	1120	86.5	5.1	826	4	US-09-877-730-16	Sequence 16, App1
1048	89	5.3	466	2	US-08-432-016-4	Sequence 4, App1	1121	86.5	5.1	885	1	US-08-372-892-4	Sequence 4, App1
1049	89	5.3	466	2	US-08-684-594-4	Sequence 4, App1	1122	86.5	5.1	885	4	US-09-519-497-52	Sequence 52, App1

1123	86.5	5.1	894	1	US-08-372-892-2	Sequence 2, Appl1	1196	84.5	5.0	457	1	US-08-416-478A-8	Sequence 8, Appl1
1124	86.5	5.1	894	1	US-08-445-640-34	Sequence 34, Appl1	1197	84.5	5.0	457	2	US-08-474-988B-8	Sequence 8, Appl1
1125	86.5	5.1	894	3	US-08-170-558-14	Sequence 34, Appl1	1198	84.5	5.0	457	2	US-08-394-442B-8	Sequence 8, Appl1
1126	86.5	5.1	894	3	US-08-447-314-34	Sequence 34, Appl1	1199	84.5	5.0	524	4	US-09-270-747-44009	Sequence 44009, A
1127	86.5	5.1	894	3	US-08-445-461-34	Sequence 34, Appl1	1200	84	5.0	223	3	US-08-811-682-8	Sequence 8, Appl1
1128	86.5	5.1	904	4	US-09-877-730-6	Sequence 6, Appl1	1201	84	5.0	230	4	US-08-467-602-223	Sequence 223, App
1129	86.5	5.1	907	4	US-09-877-730-30	Sequence 20, Appl1	1202	84	5.0	230	4	US-08-411-295F-149	Sequence 149, App
1130	86.5	5.1	985	4	US-09-877-730-10	Sequence 10, Appl1	1203	84	5.0	241	2	US-08-324-591-18	Sequence 18, Appl1
1131	86.5	5.1	991	4	US-09-877-730-12	Sequence 12, Appl1	1204	84	5.0	241	2	US-08-326-789-18	Sequence 18, Appl1
1132	86.5	5.1	1018	4	US-08-452-052-2	Sequence 2, Appl1	1205	84	5.0	245	3	US-09-069-821-5	Sequence 5, Appl1
1133	86.5	5.1	1069	4	US-09-877-730-2	Sequence 2, Appl1	1206	84	5.0	245	3	US-09-956-086-5	Sequence 5, Appl1
1134	86.5	5.1	1072	4	US-09-877-730-18	Sequence 18, Appl1	1207	84	5.0	245	4	US-09-956-087-5	Sequence 5, Appl1
1135	86.5	5.1	1150	4	US-09-877-730-8	Sequence 8, Appl1	1208	84	5.0	264	4	US-08-467-602-265	Sequence 265, App
1136	86.5	5.1	1363	4	US-09-375-248-19	Sequence 19, Appl1	1209	84	5.0	264	4	US-08-411-295F-191	Sequence 191, App
1137	86	5.1	241	3	US-08-341-018-54	Sequence 195, App	1210	84	5.0	265	4	US-09-420-592A-5	Sequence 5, Appl1
1138	86	5.1	241	3	US-08-470-335-195	Sequence 195, App	1211	84	5.0	265	4	US-09-985-442-5	Sequence 5, Appl1
1139	86	5.1	241	3	US-08-470-339-195	Sequence 195, App	1212	84	5.0	325	4	US-09-983-580-5	Sequence 5, Appl1
1140	86	5.1	241	4	US-08-467-602-389	Sequence 389, App	1213	84	5.0	333	4	US-09-684-708A-25	Sequence 25, Appl1
1141	86	5.1	241	4	US-08-411-295F-47	Sequence 47, Appl1	1214	84	5.0	386	4	US-08-467-602-281	Sequence 281, App
1142	86	5.1	270	2	US-08-652-507-2	Sequence 2, Appl1	1215	84	5.0	386	4	US-08-411-295F-207	Sequence 207, App
1143	86	5.1	398	1	US-08-091-519-2	Sequence 2, Appl1	1216	84	5.0	400	3	US-08-811-682-2	Sequence 2, Appl1
1144	86	5.1	398	1	US-08-442-043A-2	Sequence 2, Appl1	1217	84	5.0	530	3	US-08-477-460B-4	Sequence 4, Appl1
1145	86	5.1	398	1	US-09-173-151A-26	Sequence 26, Appl1	1218	84	5.0	530	3	US-08-379-516-4	Sequence 4, Appl1
1146	86	5.1	398	4	US-09-461-908-2	Sequence 2, Appl1	1219	84	5.0	530	3	US-09-329-916-4	Sequence 4, Appl1
1147	86	5.1	398	4	US-08-441-893A-2	Sequence 2, Appl1	1220	84	5.0	530	3	US-08-485-372A-4	Sequence 4, Appl1
1148	86	5.1	398	4	US-08-406-824A-8	Sequence 8, Appl1	1221	84	5.0	530	3	US-09-409-006A-4	Sequence 4, Appl1
1149	86	5.1	398	4	US-09-921-667-8	Sequence 8, Appl1	1222	84	5.0	530	4	US-08-484-681-4	Sequence 4, Appl1
1150	86	5.1	398	4	PCT-US91-03478-2	Sequence 8, Appl1	1223	84	5.0	530	4	US-09-766-995-4	Sequence 4, Appl1
1151	86	5.1	483	3	US-09-310-463-16	Sequence 2, Appl1	1224	84	5.0	530	5	PCT-US93-07422-4	Sequence 4, Appl1
1152	86	5.1	483	4	US-08-842-248A-16	Sequence 16, Appl1	1225	84	5.0	603	4	US-08-467-602-279	Sequence 279, App
1153	86	5.1	579	3	US-09-173-151A-2	Sequence 2, Appl1	1226	84	5.0	603	4	US-08-411-295F-205	Sequence 205, App
1154	86	5.1	630	4	US-09-459-522-16	Sequence 16, Appl1	1227	84	5.0	630	4	US-08-467-602-280	Sequence 280, App
1155	86	5.1	630	4	US-09-269-939A-10	Sequence 10, Appl1	1228	84	5.0	630	4	US-08-411-295F-206	Sequence 206, App
1156	86	5.1	686	3	US-09-173-151A-4	Sequence 4, Appl1	1229	83.5	4.9	100	4	US-09-858-664A-25	Sequence 25, Appl1
1157	86	5.1	1434	4	US-10-080-505-9	Sequence 9, Appl1	1230	83.5	4.9	100	4	US-10-274-978-26	Sequence 26, Appl1
1158	85.5	5.1	225	4	US-09-530-139-42	Sequence 42, Appl1	1231	83.5	4.9	211	1	US-08-168-091A-4	Sequence 4, Appl1
1159	85.5	5.1	300	1	US-07-640-029-5	Sequence 5, Appl1	1232	83.5	4.9	211	1	US-08-235-838-5	Sequence 5, Appl1
1160	85.5	5.1	300	3	US-08-439-992A-5	Sequence 5, Appl1	1233	83.5	4.9	211	2	US-08-465-473B-5	Sequence 5, Appl1
1161	85.5	5.1	302	1	US-07-640-029-6	Sequence 6, Appl1	1234	83.5	4.9	288	2	US-08-147-772-2	Sequence 2, Appl1
1162	85.5	5.1	302	1	US-07-921-807B-7	Sequence 7, Appl1	1235	83.5	4.9	288	2	US-08-456-104-6	Sequence 6, Appl1
1163	85.5	5.1	302	1	US-07-921-807B-8	Sequence 8, Appl1	1236	83.5	4.9	288	2	US-08-101-624-23	Sequence 23, Appl1
1164	85.5	5.1	302	1	US-08-441-944A-7	Sequence 7, Appl1	1237	83.5	4.9	288	2	US-08-751-767A-6	Sequence 6, Appl1
1165	85.5	5.1	302	1	US-08-441-944A-8	Sequence 8, Appl1	1238	83.5	4.9	288	3	US-08-153-262-2	Sequence 2, Appl1
1166	85.5	5.1	302	3	US-08-439-992A-6	Sequence 6, Appl1	1239	83.5	4.9	288	3	US-08-479-744A-29	Sequence 29, Appl1
1167	85.5	5.1	312	3	US-09-079-029-10	Sequence 10, Appl1	1240	83.5	4.9	288	3	US-08-280-575B-29	Sequence 29, Appl1
1168	85.5	5.1	335	4	US-09-252-991A-27567	Sequence 27567, A	1241	83.5	4.9	288	3	US-09-159-135-2	Sequence 19, Appl1
1169	85.5	5.1	403	4	US-09-638-649-5	Sequence 5, Appl1	1242	83.5	4.9	288	3	US-08-205-697A-19	Sequence 19, Appl1
1170	85.5	5.1	615	4	US-08-840-713-35	Sequence 35, Appl1	1243	83.5	4.9	288	3	US-08-702-525-19	Sequence 19, Appl1
1171	85.5	5.1	617	4	US-08-840-713-37	Sequence 37, Appl1	1244	83.5	4.9	288	3	US-09-450-198-2	Sequence 2, Appl1
1172	85.5	5.1	741	4	US-09-585-858-11	Sequence 11, Appl1	1245	83.5	4.9	288	3	US-08-403-253A-2	Sequence 2, Appl1
1173	85.5	5.1	1665	4	US-09-858-664A-2	Sequence 2, Appl1	1246	83.5	4.9	288	4	US-09-651-200-13	Sequence 13, Appl1
1174	85.5	5.1	1665	4	US-10-274-978-2	Sequence 2, Appl1	1247	83.5	4.9	288	4	US-09-667-135-34	Sequence 34, Appl1
1175	85.5	5.1	2315	4	US-09-543-681A-5434	Sequence 5434, App	1248	83.5	4.9	288	4	US-08-435-816A-2	Sequence 2, Appl1
1176	85	5.0	140	3	US-08-986-485-4	Sequence 4, Appl1	1249	83.5	4.9	288	4	US-09-425-762-29	Sequence 29, Appl1
1177	85	5.0	247	5	PCT-US94-10257A-2	Sequence 2, Appl1	1250	83.5	4.9	288	4	US-09-837-867A-19	Sequence 19, Appl1
1178	85	5.0	328	1	US-08-225-477B-5	Sequence 5, Appl1	1251	83.5	4.9	288	4	US-09-910-174A-5	Sequence 5, Appl1
1179	85	5.0	328	5	PCT-US95-04353-5	Sequence 5, Appl1	1252	83.5	4.9	288	4	US-09-620-461-5	Sequence 5, Appl1
1180	85	5.0	361	4	US-08-467-602-248	Sequence 248, App	1253	83.5	4.9	288	4	US-08-453-886A-2	Sequence 2, Appl1
1181	85	5.0	361	4	US-08-411-295F-174	Sequence 174, App	1254	83.5	4.9	288	4	US-09-206-132-6	Sequence 6, Appl1
1182	85	5.0	398	4	US-09-579-845-4	Sequence 4, Appl1	1255	83.5	4.9	288	5	PCT-US95-02576-19	Sequence 19, Appl1
1183	85	5.0	578	4	US-08-467-602-249	Sequence 249, App	1256	83.5	4.9	307	2	US-08-332-562A-83	Sequence 83, Appl1
1184	85	5.0	578	4	US-08-411-295F-175	Sequence 175, App	1257	83.5	4.9	307	2	US-08-116-778A-6	Sequence 6, Appl1
1185	85	5.0	625	4	US-08-467-602-250	Sequence 250, App	1258	83.5	4.9	307	2	US-08-474-988B-6	Sequence 6, Appl1
1186	85	5.0	625	4	US-08-411-295F-176	Sequence 176, App	1259	83.5	4.9	307	2	US-08-394-442B-6	Sequence 6, Appl1
1187	85	5.0	769	3	US-08-434-000A-10	Sequence 10, Appl1	1260	83.5	4.9	488	1	US-08-416-478A-9	Sequence 9, Appl1
1188	85	5.0	769	3	US-09-312-157-10	Sequence 10, Appl1	1261	83.5	4.9	488	2	US-08-474-988B-9	Sequence 9, Appl1
1189	85	5.0	2409	6	5180808-2	Patent No. 5180808	1262	83.5	4.9	488	2	US-08-394-442B-9	Sequence 9, Appl1
1190	84.5	5.0	119	4	US-09-858-664A-30	Sequence 30, Appl1	1263	83.5	4.9	530	4	US-08-840-713-2	Sequence 2, Appl1
1191	84.5	5.0	119	4	US-10-274-978-31	Sequence 31, Appl1	1264	83.5	4.9	637	2	US-08-235-838-14	Sequence 14, Appl1
1192	84.5	5.0	241	4	US-08-411-295F-94	Sequence 94, Appl1	1265	83.5	4.9	637	2	US-08-465-473B-14	Sequence 14, Appl1
1193	84.5	5.0	249	4	US-08-797-689-18	Sequence 18, Appl1	1266	83.5	4.9	711	1	US-08-235-838-7	Sequence 7, Appl1
1194	84.5	5.0	249	4	US-09-984-186-18	Sequence 18, Appl1	1267	83.5	4.9	711	2	US-08-465-473B-7	Sequence 7, Appl1
1195	84.5	5.0	419	6	5169835-2	Patent No. 5169835	1268	83.5	4.9	729	1	US-08-070-165F-6	Sequence 6, Appl1

1269	83.5	4.9	729	2	US-08-885-418-6	Sequence 6, Appl1	1342	82.5	4.9	253	3	US-09-166-093-17	Sequence 17, Appl1
1270	83.5	4.9	731	1	US-08-070-165F-10	Sequence 10, Appl1	1343	82.5	4.9	253	3	US-09-172-019-17	Sequence 17, Appl1
1271	83.5	4.9	731	2	US-08-885-418-10	Sequence 10, Appl1	1344	82.5	4.9	253	3	US-09-166-094-17	Sequence 17, Appl1
1272	83.5	4.9	1151	4	US-09-710-379-2448	Sequence 2448, Ap	1345	82.5	4.9	253	4	US-09-443-213-17	Sequence 17, Appl1
1273	83.5	4.9	1154	3	US-09-134-001C-3428	Sequence 3428, Ap	1346	82.5	4.9	329	4	US-09-651-200-18	Sequence 18, Appl1
1274	83.5	4.9	3858	2	US-08-876-991-2	Sequence 2, Appl1	1347	82.5	4.9	329	4	US-09-503-040-6	Sequence 6, Appl1
1275	83.5	4.9	3858	2	US-09-059-853-2	Sequence 2, Appl1	1348	82.5	4.9	352	4	US-08-467-602-239	Sequence 239, App
1276	83	4.9	222	2	US-08-190-199A-67	Sequence 67, Appl1	1349	82.5	4.9	352	4	US-08-411-295F-165	Sequence 165, App
1277	83	4.9	223	4	US-09-248-796A-23094	Sequence 23094, A	1350	82.5	4.9	449	2	US-08-482-090-11	Sequence 11, Appl1
1278	83	4.9	237	2	US-08-224-591-16	Sequence 16, Appl1	1351	82.5	4.9	450	1	US-08-105-710-7	Sequence 7, Appl1
1279	83	4.9	237	2	US-08-468-252-5	Sequence 5, Appl1	1352	82.5	4.9	450	1	US-08-365-901-7	Sequence 7, Appl1
1280	83	4.9	237	2	US-08-926-789-16	Sequence 16, Appl1	1353	82.5	4.9	450	2	US-09-007-383-15	Sequence 15, Appl1
1281	83	4.9	237	5	US-08-668-706B-5	Sequence 5, Appl1	1354	82.5	4.9	450	3	US-08-479-703A-6	Sequence 6, Appl1
1282	83	4.9	237	5	PCT-US95-10740-5	Sequence 5, Appl1	1355	82.5	4.9	504	4	US-09-270-765-43244	Sequence 43244, A
1283	83	4.9	238	4	US-09-149-476-485	Sequence 485, App	1356	82.5	4.9	504	4	US-09-270-767-44083	Sequence 44083, A
1284	83	4.9	241	1	US-07-847-743B-30	Sequence 30, Appl1	1357	82.5	4.9	551	4	US-08-896-537A-2	Sequence 2, Appl1
1285	83	4.9	241	1	US-08-456-201-30	Sequence 30, Appl1	1358	82.5	4.9	569	4	US-08-667-602-237	Sequence 237, App
1286	83	4.9	241	2	US-08-456-241-30	Sequence 30, Appl1	1359	82.5	4.9	569	4	US-08-411-295F-163	Sequence 163, App
1287	83	4.9	241	5	PCT-US92-04295A-30	Sequence 30, Appl1	1360	82.5	4.9	616	4	US-08-467-602-238	Sequence 238, App
1288	83	4.9	273	4	US-09-270-767-32843	Sequence 32843, A	1361	82.5	4.9	616	4	US-08-411-295F-164	Sequence 164, App
1289	83	4.9	273	4	US-09-270-767-48060	Sequence 48060, A	1362	82.5	4.9	645	3	US-08-753-007A-10	Sequence 10, Appl1
1290	83	4.9	280	3	US-08-341-018-56	Sequence 56, Appl1	1363	82.5	4.9	645	3	US-09-398-496-10	Sequence 10, Appl1
1291	83	4.9	280	3	US-08-470-335-192	Sequence 192, App	1364	82.5	4.9	710	3	US-09-171-461-16	Sequence 16, Appl1
1292	83	4.9	280	3	US-08-470-339-192	Sequence 192, App	1365	82.5	4.9	710	4	US-09-970-711-16	Sequence 16, Appl1
1293	83	4.9	280	4	US-08-467-602-386	Sequence 386, App	1366	82.5	4.9	757	3	US-08-434-000A-6	Sequence 6, Appl1
1294	83	4.9	280	4	US-08-411-295F-95	Sequence 95, Appl1	1367	82.5	4.9	757	4	US-09-312-157-6	Sequence 6, Appl1
1295	83	4.9	281	1	US-08-487-748A-9	Sequence 9, Appl1	1368	82	4.9	210	4	US-08-467-602-215	Sequence 215, Appl1
1296	83	4.9	281	1	US-08-487-748A-10	Sequence 10, Appl1	1369	82	4.9	210	4	US-08-411-295F-141	Sequence 141, App
1297	83	4.9	281	3	US-08-480-070C-10	Sequence 10, Appl1	1370	82	4.9	226	4	US-09-869-388-10	Sequence 10, Appl1
1298	83	4.9	281	3	US-08-829-525-10	Sequence 10, Appl1	1371	82	4.9	244	4	US-08-467-602-257	Sequence 257, App
1299	83	4.9	281	3	US-08-609-583A-10	Sequence 10, Appl1	1372	82	4.9	244	4	US-08-411-295F-183	Sequence 183, App
1300	83	4.9	281	3	US-08-317-399-10	Sequence 10, Appl1	1373	82	4.9	290	4	US-09-910-174B-8	Sequence 8, Appl1
1301	83	4.9	281	4	US-09-310-367-10	Sequence 10, Appl1	1374	82	4.9	290	4	US-09-620-461-8	Sequence 8, Appl1
1302	83	4.9	281	4	US-09-032-337-10	Sequence 10, Appl1	1375	82	4.9	474	4	US-09-828-995B-17	Sequence 17, Appl1
1303	83	4.9	281	4	US-09-464-331-10	Sequence 10, Appl1	1376	82	4.9	522	4	US-09-549-513-33	Sequence 33, Appl1
1304	83	4.9	281	3	US-09-361-434-17	Sequence 17, Appl1	1377	82	4.9	535	3	US-08-983-035A-18	Sequence 18, Appl1
1305	83	4.9	321	3	US-09-361-434-22	Sequence 22, Appl1	1378	82	4.9	590	4	US-09-520-781-12	Sequence 12, Appl1
1306	83	4.9	321	3	US-09-635-025-17	Sequence 17, Appl1	1379	82	4.9	661	2	US-08-795-868-14	Sequence 14, Appl1
1307	83	4.9	321	3	US-09-635-025-22	Sequence 22, Appl1	1380	82	4.9	661	3	US-09-303-066-14	Sequence 14, Appl1
1308	83	4.9	321	4	US-09-222-938A-64	Sequence 64, Appl1	1381	82	4.9	661	3	US-09-134-250-14	Sequence 14, Appl1
1309	83	4.9	370	4	US-09-479-614-14	Sequence 14, Appl1	1382	81.5	4.8	214	3	US-09-247-352-4	Sequence 4, Appl1
1310	83	4.9	411	4	US-09-583-110-4414	Sequence 4414, Ap	1383	81.5	4.8	214	4	US-09-466-635-4	Sequence 4, Appl1
1311	83	4.9	445	4	US-09-479-614-2	Sequence 2, Appl1	1384	81.5	4.8	239	3	US-08-279-772A-8	Sequence 8, Appl1
1312	83	4.9	445	4	US-09-479-614-29	Sequence 29, Appl1	1385	81.5	4.8	239	3	US-08-902-486-11	Sequence 11, Appl1
1313	83	4.9	484	4	US-09-354-151-2	Sequence 2, Appl1	1386	81.5	4.8	268	4	US-09-976-118-1	Sequence 1, Appl1
1314	83	4.9	539	1	US-08-463-163-3	Sequence 3, Appl1	1387	81.5	4.8	326	4	US-09-248-796A-14157	Sequence 14157, A
1315	83	4.9	645	1	US-07-847-743B-27	Sequence 27, Appl1	1388	81.5	4.8	602	2	US-08-795-868-16	Sequence 16, Appl1
1316	83	4.9	645	1	US-08-456-201-27	Sequence 27, Appl1	1389	81.5	4.8	602	3	US-09-303-069-16	Sequence 16, Appl1
1317	83	4.9	645	1	US-08-428-926-4	Sequence 4, Appl1	1390	81.5	4.8	661	1	US-09-134-250-16	Sequence 12, Appl1
1318	83	4.9	645	1	US-08-428-927-4	Sequence 4, Appl1	1391	81.5	4.8	661	2	US-08-232-538-12	Sequence 12, Appl1
1319	83	4.9	645	1	US-08-339-517-4	Sequence 4, Appl1	1392	81.5	4.8	687	1	US-08-232-538-6	Sequence 6, Appl1
1320	83	4.9	645	2	US-08-456-241-27	Sequence 27, Appl1	1393	81.5	4.8	687	2	US-08-786-164-6	Sequence 6, Appl1
1321	83	4.9	645	3	US-09-020-880-93	Sequence 93, Appl1	1394	81.5	4.8	687	3	US-09-427-353-2	Sequence 2, Appl1
1322	83	4.9	645	3	US-09-101-544-93	Sequence 93, Appl1	1395	81.5	4.8	1188	1	US-08-201-697-4	Sequence 4, Appl1
1323	83	4.9	645	3	US-09-097-681-3	Sequence 3, Appl1	1396	81	4.8	87	4	US-09-858-664A-29	Sequence 29, Appl1
1325	83	4.9	645	5	PCT-US92-04295A-27	Sequence 27, Appl1	1397	81	4.8	87	4	US-10-274-978-30	Sequence 30, Appl1
1326	83	4.9	722	1	US-07-847-743B-9	Sequence 9, Appl1	1398	81	4.8	227	4	US-09-869-388-6	Sequence 6, Appl1
1327	83	4.9	722	1	US-08-456-201-9	Sequence 9, Appl1	1399	81	4.8	235	3	US-09-485-737B-93	Sequence 93, Appl1
1328	83	4.9	722	2	US-08-456-241-9	Sequence 9, Appl1	1400	81	4.8	239	4	US-09-828-995B-26	Sequence 26, Appl1
1329	83	4.9	722	2	US-08-456-241-9	Sequence 9, Appl1	1401	81	4.8	401	6	5252556-1	Patent No. 5252556
1330	83	4.9	722	5	PCT-US92-04295A-9	Sequence 9, Appl1	1402	81	4.8	476	4	US-09-291-299A-3	Sequence 3, Appl1
1331	83	4.9	218	4	US-10-026-045-1	Sequence 1, Appl1	1403	81	4.8	945	4	US-10-140-000-146	Sequence 146, App
1332	82.5	4.9	244	1	US-08-230-843-2	Sequence 2, Appl1	1404	81	4.8	90	3	US-08-928-383B-22	Sequence 22, Appl1
1333	82.5	4.9	244	2	US-08-636-936-2	Sequence 2, Appl1	1405	80.5	4.8	129	4	US-09-556-605-2	Sequence 33, Appl1
1334	82.5	4.9	250	2	US-08-392-338A-15	Sequence 15, Appl1	1406	80.5	4.8	165	1	US-08-168-091A-33	Sequence 32640, A
1335	82.5	4.9	250	3	US-09-166-750-15	Sequence 15, Appl1	1407	80.5	4.8	191	4	US-09-270-767-33640	Sequence 2, Appl1
1336	82.5	4.9	250	3	US-09-166-093-15	Sequence 15, Appl1	1408	80.5	4.8	206	3	US-08-341-018-2	Sequence 190, App
1337	82.5	4.9	250	3	US-09-172-019-15	Sequence 15, Appl1	1409	80.5	4.8	206	3	US-08-470-338-100	Sequence 190, App
1338	82.5	4.9	250	3	US-09-166-094-15	Sequence 15, Appl1	1410	80.5	4.8	206	3	US-08-467-602-353	Sequence 383, App
1339	82.5	4.9	250	4	US-09-443-213-15	Sequence 15, Appl1	1411	80.5	4.8	206	4	US-08-411-295F-2	Sequence 2, Appl1
1340	82.5	4.9	253	3	US-08-392-338A-17	Sequence 17, Appl1	1412	80.5	4.8	206	4	US-08-411-295F-2	Sequence 2, Appl1
1341	82.5	4.9	253	3	US-09-166-750-17	Sequence 17, Appl1	1413	80.5	4.8	206	4	US-08-411-295F-76	Sequence 76, Appl1

Db 241 TEAPTTMYPLKATSTVKOSWMTTMDGYLGSETSAGPKSLPVFAIIILISLCMVVFT 300
QY 301 MAIYMLCRKTSQOEHYEAR 321
Db 301 MAIYMLCRKTSQOEHYEAR 321

RESULT 2
US-09-369-247-63

/ Sequence 63, Application US/09369247
/ Patent No. 6563992
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: 44 Human Secreted Proteins
/ FILE REFERENCE: P2024P1
/ CURRENT APPLICATION NUMBER: US/09/369,247
/ EARLIER FILING DATE: 1999-08-05
/ EARLIER APPLICATION NUMBER: 60/074,118
/ EARLIER FILING DATE: 1998-02-09
/ EARLIER APPLICATION NUMBER: 60/074,157
/ EARLIER FILING DATE: 1998-02-09
/ EARLIER APPLICATION NUMBER: 60/074,137
/ EARLIER FILING DATE: 1998-02-09
/ EARLIER APPLICATION NUMBER: 60/074,341
/ EARLIER FILING DATE: 1998-02-09
/ EARLIER APPLICATION NUMBER: 60/074,141
/ EARLIER FILING DATE: 1998-02-09
/ NUMBER OF SEQ ID NOS: 172
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 63
/ LENGTH: 306
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (306)
/ OTHER INFORMATION: Xaa equals stop translation
US-09-369-247-63

Query Match

Best local Similarity 67.4%; Score 1137; DB 4; Length 306;
Matches 226; Conservative 0; Mismatches 1; Indels 94; Gaps 1;

QY 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPMKGDVNLPCYTDPLQGYTVLVKMLVGR 60
Db 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPMKGDVNLPCYTDPLQGYTVLVKMLVGR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRLVSHKVPDVSLSLSTLEMDRSHYTCVWTQTP 120
Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRLVSHKVPDVSLSLSTLEMDRSHYTCVWTQTP 120
QY 121 DGNQVVRDKTELRVQKLSVSKRTVTGSGYGFVQGMKRLISLQCAQSGSPISYIWMYQ 180
Db 121 DGNQVVRDKTELRVQKLSVSKRTVTGSGYGFVQGMKRLISLQCAQSGSPISYIWMYQ 180
QY 121 DGNQVVRDKTELRVQKLSVSKRTVTGSGYGFVQGMKRLISLQCAQSGSPISYIWMYQ 180
Db 121 DGNQVVRDKTELRVQKLSVSKRTVTGSGYGFVQGMKRLISLQCAQSGSPISYIWMYQ 180
QY 181 QTNNOPIKAVATLSTLFFKPAVIADSGSYFCTAKQGVSGEBSHDIVKVFYKDSKLLKTK 240
Db 181 QTNNOPIKAVATLSTLFFKPAVIADSGSYFCTAKQGVSGEBSHDIVKVFYKDSKLLKTK 240
QY 137 -----KISSKLLKTK 146
Db 137 -----KISSKLLKTK 146
QY 241 TEAPTTMYPLKATSTVKOSWMTTMDGYLGSETSAGPKSLPVFAIIILISLCMVVFT 300
Db 147 TEAPTTMYPLKATSTVKOSWMTTMDGYLGSETSAGPKSLPVFAIIILISLCMVVFT 300
QY 301 MAIYMLCRKTSQOEHYEAR 321
Db 207 MAIYMLCRKTSQOEHYEAR 227

RESULT 3
US-09-188-930-189

/ Sequence 189, Application US/09188930A
/ Patent No. 6150502
/ GENERAL INFORMATION:

/ APPLICANT: Watson, James D.
/ APPLICANT: Strachan, Lorna
/ APPLICANT: Sleeman, Matthew
/ APPLICANT: Onrust, Rene
/ APPLICANT: Murison, James Greg
/ TITLE OF INVENTION: Compositions Isolated From Skin Cells
/ FILE REFERENCE: 11000.1011c1
/ CURRENT APPLICATION NUMBER: US/09/188,930A
/ CURRENT FILING DATE: 1998-11-09
/ NUMBER OF SEQ ID NOS: 348
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 189
/ LENGTH: 299
/ TYPE: PRT
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (247)...(247)
/ NAME/KEY: UNSURE
/ LOCATION: (289)...(289)
US-09-188-930-189

Query Match

Best local Similarity 10.6%; Score 178.5; DB 3; Length 299;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPMKGDVNLPCYTDPLQGYTVLVKMLVGR 60
Db 17 LAILCSLALGSVTVHS--SEPERIPEN-----NPVKLSCAV---SGSPRVEW----- 62
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRLVSHK-----VPDVSLSLSTLEMDRSHYTCV 115
Db 63 -----KPDGDTTRVLCVNNKITASVEDRVTFPLPGIIFPKSVTRB--DRTYTCMV 111
QY 116 TWQTPDGNQVVRDKTELRVQKLSVSKRTVTGSGYGFVQGMKRLISLQCAQSGSPIS 174
Db 112 SEEGNSYGEVAKLIVL-----VPSKPTVNIPS-----SATIGNRAVLTCSEDDGSPPE 163
QY 175 YIWMYK-----QQTN-----NOEPIKAVATLSTLFFKPAVIADSGSYFCTAKQGVSEQH 222
Db 164 YTFPDKGIVMPTNPKSTRAPNSSYVNLPTGELVFDPLASDGTGHSCEARNGYGTPT 223
QY 223 SDIVK 227
Db 224 SNAVR 228

RESULT 4

US-09-188-930-331
/ Sequence 331, Application US/09188930A
/ Patent No. 6150502
/ GENERAL INFORMATION:

/ APPLICANT: Watson, James D.
/ APPLICANT: Strachan, Lorna
/ APPLICANT: Sleeman, Matthew
/ APPLICANT: Onrust, Rene
/ APPLICANT: Murison, James Greg
/ TITLE OF INVENTION: Compositions Isolated From Skin Cells
/ FILE REFERENCE: 11000.1011c1
/ CURRENT APPLICATION NUMBER: US/09/188,930A
/ CURRENT FILING DATE: 1998-11-09
/ NUMBER OF SEQ ID NOS: 348
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 331
/ LENGTH: 299
/ TYPE: PRT
/ ORGANISM: Human
US-09-188-930-331

Query Match

Best local Similarity 10.6%; Score 178.5; DB 3; Length 299;
Matches 26.5%; Pred. No. 7.3e-10;

LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-189

Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 7.3e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLLGHLTVDTYGRPLIEVESVTPGPKGDVNPCTYDPLQGYQVLYKVLVQR 60
DB 17 LAILLCSLALGSVTYVHS--SEPEFRIPEN-----NPVKLSCAV---SGFSPREWE----- 62
QY 61 GSDPVTIPLRDSGSDHIQQAQYQGRILVSHK-----VPGDVSQQLSTLEMDRSHYTCVEY 115
DB 63 -----KFDGDDTTLVLCVNNKKTASVEDRVTLPGITFKSYTR--DIGYTTCAV 111
QY 116 TWQTPDGNNOVVRDKITELRVQKLSVSKPTVTTSGSGYGFVPGQMRISLQCAR-GSPPIIS 174
DB 112 SEEGSGSYGEVKVYKLIYL-----VPPSKPTVINIPS-----SATIGNRAVLTCSEQDGSPPSE 163
QY 175 YIMYK-----QQTN-----NOEPIKVAATLSTLTKFRPANIADSGSYFCTAKQVQSEQH 222
DB 164 YIMFKDGIYVMPINPKSTRAFSNSSYVLANPTTGBLVDPDLSADTGEYSCEARNGYGTPTMT 223
QY 223 SDIVK 227
DB 224 SNAVR 228

RESULT 8
US-09-312-283C-331
Sequence 331, Application US/09312283C
Patent No. 6573095

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murlison, James G.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: ParseSeq for Windows Version 4.0
SEQ ID NO 331
LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-331

Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 7.3e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLLGHLTVDTYGRPLIEVESVTPGPKGDVNPCTYDPLQGYQVLYKVLVQR 60
DB 17 LAILLCSLALGSVTYVHS--SEPEFRIPEN-----NPVKLSCAV---SGFSPREWE----- 62
QY 61 GSDPVTIPLRDSGSDHIQQAQYQGRILVSHK-----VPGDVSQQLSTLEMDRSHYTCVEY 115
DB 63 -----KFDGDDTTLVLCVNNKKTASVEDRVTLPGITFKSYTR--DIGYTTCAV 111
QY 116 TWQTPDGNNOVVRDKITELRVQKLSVSKPTVTTSGSGYGFVPGQMRISLQCAR-GSPPIIS 174
DB 112 SEEGSGSYGEVKVYKLIYL-----VPPSKPTVINIPS-----SATIGNRAVLTCSEQDGSPPSE 163
QY 175 YIMYK-----QQTN-----NOEPIKVAATLSTLTKFRPANIADSGSYFCTAKQVQSEQH 222
DB 164 YIMFKDGIYVMPINPKSTRAFSNSSYVLANPTTGBLVDPDLSADTGEYSCEARNGYGTPTMT 223

QY 223 SDIVK 227
DB 224 SNAVR 228

RESULT 9
US-09-907-794A-119
Sequence 119, Application US/09907794A
Patent No. 6635468

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertschen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20

```

; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-119

Query Match      10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 7.3e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLGLHLYDVGRIPLVPSVYGPVKGDVNLCTYDPLQGYQVLVKNLVQR 60
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 17 LAILLCSLALGSVTVHS-SEPEVRIPEH-----NPKLSCAY---SGFSSPRVEM---- 62
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 GSDPVITFLRDSGDHIIQAKYQGRLLVSHK-----VPGDVSLQLSTLEMDRSHYTCV 115
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 63 -----KFDGDTTRLVLCYNNKITAASYEDRVTFPLTGITPKSVTR--DTGYTCMV 111
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 116 TWQTPDGNQVVRKITEFLRVQKLSVKPYTTTSGSGYGFVYPOGMRISLQCGAR-GSPPI 174
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 112 SEEGGNSYGEVKKVLYLVL-----VPPSKPTVNIPS-----SATIGNRAVLTCSEODGSPSE 163
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 175 YIYWK-----QQTN-----NOEPIKVAITLSTLFFKPAVIADSGSYFCTAKGVGSEQH 222
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 164 YTFWKDGIWMPTRPKSTRAFSNNSYVLPFTTGLVDFPLASDGTGEYSCARNGYGTPTMT 223
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 223 SDIYK 227
   :|||:
DB 224 SNAVR 228
```

RESULT 10
US-09-905-125A-119
; Sequence 119, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Batton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07

US-09-905-125A-119
; Sequence 119, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Batton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07

```

; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-119

Query Match      10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 7.3e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLGLHLYDVGRIPLVPSVYGPVKGDVNLCTYDPLQGYQVLVKNLVQR 60
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 17 LAILLCSLALGSVTVHS-SEPEVRIPEH-----NPKLSCAY---SGFSSPRVEM---- 62
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 GSDPVITFLRDSGDHIIQAKYQGRLLVSHK-----VPGDVSLQLSTLEMDRSHYTCV 115
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 63 -----KFDGDTTRLVLCYNNKITAASYEDRVTFPLTGITPKSVTR--DTGYTCMV 111
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 116 TWQTPDGNQVVRKITEFLRVQKLSVKPYTTTSGSGYGFVYPOGMRISLQCGAR-GSPPI 174
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 112 SEEGGNSYGEVKKVLYLVL-----VPPSKPTVNIPS-----SATIGNRAVLTCSEODGSPSE 163
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 175 YIYWK-----QQTN-----NOEPIKVAITLSTLFFKPAVIADSGSYFCTAKGVGSEQH 222
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 164 YTFWKDGIWMPTRPKSTRAFSNNSYVLPFTTGLVDFPLASDGTGEYSCARNGYGTPTMT 223
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 223 SDIYK 227
   :|||:
DB 224 SNAVR 228
```

US-09-902-775A-119
; Sequence 119, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Batton, Dan L.
; APPLICANT: Ferrara, Napoleone

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 06:08:47 ; Search time 539 Seconds

(without alignments)
214.235 Million cell updates/sec

Title: US-10-767-374-2

Perfect score: 1688
Sequence: 1 MGILLGLLGLHGLTVDYGR.....AYIMLCRKTSQGEHYVEAAR 321

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1688	100.0	321	9	US-09-978-285A-52
2	1688	100.0	321	9	US-09-978-687-52
3	1688	100.0	321	9	US-09-978-192A-52
4	1688	100.0	321	9	US-09-953-499-2
5	1688	100.0	321	9	US-09-999-832A-52
6	1688	100.0	321	10	US-09-978-189-52
7	1688	100.0	321	10	US-09-978-608A-52
8	1688	100.0	321	10	US-09-978-585A-52
9	1688	100.0	321	10	US-09-978-191A-52
10	1688	100.0	321	10	US-09-978-403A-52
11	1688	100.0	321	10	US-09-978-564A-52
12	1688	100.0	321	10	US-09-999-833A-52
13	1688	100.0	321	10	US-09-981-915A-52

14	1688	100.0	321	10	US-09-978-824-52	Sequence 52, App1
15	1688	100.0	321	10	US-09-918-585A-52	Sequence 52, App1
16	1688	100.0	321	10	US-09-999-834A-52	Sequence 52, App1
17	1688	100.0	321	10	US-09-978-423A-52	Sequence 52, App1
18	1688	100.0	321	10	US-09-978-193A-52	Sequence 52, App1
19	1688	100.0	321	10	US-09-999-830A-52	Sequence 52, App1
20	1688	100.0	321	10	US-09-978-757A-52	Sequence 52, App1
21	1688	100.0	321	10	US-09-978-187B-52	Sequence 52, App1
22	1688	100.0	321	10	US-09-978-643A-52	Sequence 52, App1
23	1688	100.0	321	10	US-09-978-375A-52	Sequence 52, App1
24	1688	100.0	321	10	US-09-978-298A-52	Sequence 52, App1
25	1688	100.0	321	10	US-09-978-188A-52	Sequence 52, App1
26	1688	100.0	321	10	US-09-978-681A-52	Sequence 52, App1
27	1688	100.0	321	10	US-09-978-194A-52	Sequence 52, App1
28	1688	100.0	321	10	US-09-999-829A-52	Sequence 52, App1
29	1688	100.0	321	10	US-09-978-299A-52	Sequence 52, App1
30	1688	100.0	321	10	US-09-978-544A-52	Sequence 52, App1
31	1688	100.0	321	10	US-09-978-665A-52	Sequence 52, App1
32	1688	100.0	321	10	US-09-978-802A-52	Sequence 52, App1
33	1688	100.0	321	11	US-09-899-831A-52	Sequence 52, App1
34	1688	100.0	321	14	US-10-017-081A-52	Sequence 52, App1
35	1688	100.0	321	14	US-10-167-749-52	Sequence 52, App1
36	1688	100.0	321	14	US-10-013-921A-52	Sequence 52, App1
37	1688	100.0	321	14	US-10-013-929A-52	Sequence 52, App1
38	1688	100.0	321	14	US-10-016-177A-52	Sequence 52, App1
39	1688	100.0	321	14	US-10-166-709A-52	Sequence 52, App1
40	1688	100.0	321	14	US-10-143-031A-52	Sequence 52, App1
41	1688	100.0	321	14	US-10-143-030A-52	Sequence 52, App1
42	1688	100.0	321	14	US-10-002-967A-52	Sequence 52, App1
43	1688	100.0	321	14	US-10-017-083A-52	Sequence 52, App1
44	1688	100.0	321	14	US-10-145-128A-52	Sequence 52, App1
45	1688	100.0	321	14	US-10-017-191A-52	Sequence 52, App1
46	1688	100.0	321	14	US-10-265-542-2	Sequence 2, App1
47	1688	100.0	321	14	US-10-143-028A-52	Sequence 52, App1
48	1688	100.0	321	14	US-10-143-029A-52	Sequence 52, App1
49	1688	100.0	321	14	US-10-145-089A-52	Sequence 52, App1
50	1688	100.0	321	14	US-10-165-067A-52	Sequence 52, App1
51	1688	100.0	321	14	US-10-145-017A-52	Sequence 52, App1
52	1688	100.0	321	14	US-10-164-728A-52	Sequence 52, App1
53	1688	100.0	321	14	US-10-013-926A-52	Sequence 52, App1
54	1688	100.0	321	14	US-10-165-247A-52	Sequence 52, App1
55	1688	100.0	321	14	US-10-145-124A-52	Sequence 52, App1
56	1688	100.0	321	14	US-10-160-502A-52	Sequence 52, App1
57	1688	100.0	321	14	US-10-145-087A-52	Sequence 52, App1
58	1688	100.0	321	14	US-10-017-086A-52	Sequence 52, App1
59	1688	100.0	321	14	US-10-164-829A-52	Sequence 52, App1
60	1688	100.0	321	14	US-10-164-829A-52	Sequence 52, App1
61	1688	100.0	321	14	US-10-145-092A-52	Sequence 52, App1
62	1688	100.0	321	14	US-10-020-445A-52	Sequence 52, App1
63	1688	100.0	321	14	US-10-013-924A-52	Sequence 52, App1
64	1688	100.0	321	14	US-10-017-084A-52	Sequence 52, App1
65	1688	100.0	321	14	US-10-145-016A-52	Sequence 52, App1
66	1688	100.0	321	14	US-10-145-088A-52	Sequence 52, App1
67	1688	100.0	321	14	US-10-145-092A-52	Sequence 52, App1
68	1688	100.0	321	14	US-10-145-129A-52	Sequence 52, App1
69	1688	100.0	321	14	US-10-165-038A-52	Sequence 52, App1
70	1688	100.0	321	14	US-10-165-353A-52	Sequence 52, App1
71	1688	100.0	321	14	US-10-167-600-52	Sequence 52, App1
72	1688	100.0	321	14	US-10-170-481A-52	Sequence 52, App1
73	1688	100.0	321	14	US-10-172-039A-52	Sequence 52, App1
74	1688	100.0	321	14	US-10-210-028A-52	Sequence 52, App1
75	1688	100.0	321	14	US-10-017-085A-52	Sequence 52, App1
76	1688	100.0	321	14	US-10-013-916A-52	Sequence 52, App1
77	1688	100.0	321	14	US-10-143-026A-52	Sequence 52, App1
78	1688	100.0	321	14	US-10-013-918A-52	Sequence 52, App1
79	1688	100.0	321	14	US-10-162-521A-52	Sequence 52, App1
80	1688	100.0	321	14	US-10-013-928A-52	Sequence 52, App1
81	1688	100.0	321	14	US-10-162-522A-52	Sequence 52, App1
82	1688	100.0	321	14	US-10-013-923A-52	Sequence 52, App1
83	1688	100.0	321	14	US-10-013-925A-52	Sequence 52, App1
84	1688	100.0	321	14	US-10-013-927A-52	Sequence 52, App1
85	1688	100.0	321	15	US-10-145-093A-52	Sequence 52, App1
86	1688	100.0	321	15	US-10-013-919A-52	Sequence 52, App1

87	1688	100.0	321	15	US-10-013-920A-52	Sequence 52, Appl	160	178.5	10.6	299	10	US-09-903-882-119	Sequence 119, App
88	1688	100.0	321	15	US-10-164-749A-52	Sequence 52, Appl	161	178.5	10.6	299	10	US-09-907-652-119	Sequence 119, App
89	1688	100.0	321	15	US-10-013-917A-52	Sequence 52, Appl	162	178.5	10.6	299	10	US-09-902-572A-119	Sequence 119, App
90	1688	100.0	321	16	US-10-633-008-2	Sequence 2, Appl1	163	178.5	10.6	299	10	US-09-902-979-119	Sequence 119, App
91	1688	100.0	321	16	US-10-785-220-2	Sequence 2, Appl1	164	178.5	10.6	299	10	US-09-905-125-119	Sequence 119, App
92	1688	100.0	321	16	US-10-785-221-2	Sequence 2, Appl1	165	178.5	10.6	299	10	US-09-906-815A-119	Sequence 119, App
93	1688	100.0	321	16	US-10-785-433-2	Sequence 2, Appl1	166	178.5	10.6	299	10	US-09-905-444-119	Sequence 119, App
94	1688	100.0	321	17	US-10-152-388B-52	Sequence 52, Appl1	167	178.5	10.6	299	10	US-09-903-806-119	Sequence 119, App
95	1688	100.0	321	17	US-10-767-374-2	Sequence 2, Appl1	168	178.5	10.6	299	10	US-09-904-992-119	Sequence 119, App
96	1688	100.0	321	17	US-10-785-607-2	Sequence 2, Appl1	169	178.5	10.6	299	10	US-09-904-838-119	Sequence 119, App
97	1688	100.0	399	11	US-09-833-245-1236	Sequence 1236, App	170	178.5	10.6	299	10	US-09-906-777-119	Sequence 119, App
98	1688	100.0	399	11	US-09-833-245-1237	Sequence 1237, App	171	178.5	10.6	299	10	US-09-903-603A-119	Sequence 119, App
99	1688	100.0	399	15	US-10-458-113-8	Sequence 8, Appl1	172	178.5	10.6	299	10	US-09-904-532-119	Sequence 119, App
100	1688	100.0	399	15	US-10-211-462-225	Sequence 225, Appl	173	178.5	10.6	299	10	US-09-904-766-119	Sequence 119, App
101	1688	100.0	399	16	US-10-633-008-32	Sequence 32, Appl	174	178.5	10.6	299	10	US-09-904-920A-119	Sequence 119, App
102	1688	100.0	399	16	US-10-656-269-42	Sequence 42, Appl	175	178.5	10.6	299	10	US-09-904-877A-119	Sequence 119, App
103	1480	87.7	281	16	US-10-656-269-44	Sequence 44, Appl	176	178.5	10.6	299	10	US-09-903-562-119	Sequence 119, App
104	1137	67.4	305	16	US-10-633-008-33	Sequence 33, Appl	177	178.5	10.6	299	10	US-09-906-618-119	Sequence 119, App
105	1137	67.4	306	16	US-10-062-548-33	Sequence 63, Appl	178	178.5	10.6	299	10	US-09-907-728-119	Sequence 119, App
106	728	43.1	280	16	US-10-633-008-34	Sequence 34, Appl	179	178.5	10.6	299	10	US-09-904-805-119	Sequence 119, App
107	728	43.1	280	16	US-10-656-269-14	Sequence 14, Appl	180	178.5	10.6	299	10	US-09-906-722A-119	Sequence 119, App
108	613	36.3	188	16	US-10-656-269-16	Sequence 16, Appl	181	178.5	10.6	299	10	US-09-906-928A-119	Sequence 119, App
109	178.5	10.6	299	9	US-09-799-777-51	Sequence 51, Appl	182	178.5	10.6	299	11	US-09-908-576-119	Sequence 119, App
110	178.5	10.6	299	9	US-09-909-320-119	Sequence 119, App	183	178.5	10.6	299	11	US-09-833-245-1300	Sequence 1300, App
111	178.5	10.6	299	9	US-09-909-088B-119	Sequence 119, App	184	178.5	10.6	299	11	US-09-833-245-1301	Sequence 1301, App
112	178.5	10.6	299	9	US-09-905-291A-119	Sequence 119, App	185	178.5	10.6	299	13	US-10-026-500-91	Sequence 91, Appl
113	178.5	10.6	299	9	US-09-953-499-1	Sequence 1, Appl1	186	178.5	10.6	299	14	US-10-028-072-366	Sequence 366

233	178.5	10.6	299	14	US-10-131-824A-366	Sequence 366, App	366	178.5	10.6	299	14	US-10-127-832A-366	Sequence 366, App
234	178.5	10.6	299	14	US-10-131-830A-366	Sequence 366, App	367	178.5	10.6	299	14	US-10-127-833A-366	Sequence 366, App
235	178.5	10.6	299	14	US-10-131-837A-366	Sequence 366, App	308	178.5	10.6	299	14	US-10-127-834A-366	Sequence 366, App
236	178.5	10.6	299	14	US-10-137-872A-366	Sequence 366, App	309	178.5	10.6	299	14	US-10-127-836A-366	Sequence 366, App
237	178.5	10.6	299	14	US-10-147-500A-366	Sequence 366, App	310	178.5	10.6	299	14	US-10-127-841A-366	Sequence 366, App
238	178.5	10.6	299	14	US-10-147-502A-366	Sequence 366, App	311	178.5	10.6	299	14	US-10-127-844A-366	Sequence 366, App
239	178.5	10.6	299	14	US-10-147-515A-366	Sequence 366, App	312	178.5	10.6	299	14	US-10-128-687A-366	Sequence 366, App
240	178.5	10.6	299	14	US-10-147-517A-366	Sequence 366, App	313	178.5	10.6	299	14	US-10-128-688A-366	Sequence 366, App
241	178.5	10.6	299	14	US-10-147-526A-366	Sequence 366, App	314	178.5	10.6	299	14	US-10-128-689A-366	Sequence 366, App
242	178.5	10.6	299	14	US-10-147-527A-366	Sequence 366, App	315	178.5	10.6	299	14	US-10-128-694A-366	Sequence 366, App
243	178.5	10.6	299	14	US-10-121-041A-366	Sequence 366, App	316	178.5	10.6	299	14	US-10-131-825A-366	Sequence 366, App
244	178.5	10.6	299	14	US-10-121-043A-366	Sequence 366, App	317	178.5	10.6	299	14	US-10-130-417A-366	Sequence 366, App
245	178.5	10.6	299	14	US-10-121-047A-366	Sequence 366, App	318	178.5	10.6	299	14	US-10-131-815A-366	Sequence 366, App
246	178.5	10.6	299	14	US-10-123-215A-366	Sequence 366, App	319	178.5	10.6	299	14	US-10-131-817A-366	Sequence 366, App
247	178.5	10.6	299	14	US-10-123-902A-366	Sequence 366, App	320	178.5	10.6	299	14	US-10-131-821A-366	Sequence 366, App
248	178.5	10.6	299	14	US-10-123-908A-366	Sequence 366, App	321	178.5	10.6	299	14	US-10-131-822A-366	Sequence 366, App
249	178.5	10.6	299	14	US-10-123-909A-366	Sequence 366, App	322	178.5	10.6	299	14	US-10-131-828A-366	Sequence 366, App
250	178.5	10.6	299	14	US-10-123-910A-366	Sequence 366, App	323	178.5	10.6	299	14	US-10-131-835A-366	Sequence 366, App
251	178.5	10.6	299	14	US-10-124-813A-366	Sequence 366, App	324	178.5	10.6	299	14	US-10-137-869A-366	Sequence 366, App
252	178.5	10.6	299	14	US-10-124-817A-366	Sequence 366, App	325	178.5	10.6	299	14	US-10-137-864A-366	Sequence 366, App
253	178.5	10.6	299	14	US-10-125-922A-366	Sequence 366, App	326	178.5	10.6	299	14	US-10-147-523A-366	Sequence 366, App
254	178.5	10.6	299	14	US-10-125-924A-366	Sequence 366, App	327	178.5	10.6	299	14	US-10-158-785A-366	Sequence 366, App
255	178.5	10.6	299	14	US-10-140-860A-366	Sequence 366, App	328	178.5	10.6	299	14	US-10-121-051A-366	Sequence 366, App
256	178.5	10.6	299	14	US-10-142-417A-366	Sequence 366, App	329	178.5	10.6	299	14	US-10-121-042A-366	Sequence 366, App
257	178.5	10.6	299	14	US-10-147-519A-366	Sequence 366, App	330	178.5	10.6	299	14	US-10-123-912A-366	Sequence 366, App
258	178.5	10.6	299	14	US-10-157-782A-366	Sequence 366, App	331	178.5	10.6	299	14	US-10-123-085A-54	Sequence 54, App1
259	178.5	10.6	299	14	US-10-157-783A-366	Sequence 366, App	332	178.5	10.6	299	14	US-10-123-085A-54	Sequence 366, App
260	178.5	10.6	299	14	US-10-127-842A-366	Sequence 366, App	333	178.5	10.6	299	14	US-10-194-359A-366	Sequence 366, App
261	178.5	10.6	299	14	US-10-125-926A-366	Sequence 366, App	334	178.5	10.6	299	14	US-10-126-739A-91	Sequence 91, App1
262	178.5	10.6	299	14	US-10-125-930A-366	Sequence 366, App	335	178.5	10.6	299	14	US-10-123-084A-54	Sequence 54, App1
263	178.5	10.6	299	14	US-10-127-831A-366	Sequence 366, App	336	178.5	10.6	299	14	US-10-123-080A-54	Sequence 54, App1
264	178.5	10.6	299	14	US-10-127-837A-366	Sequence 366, App	337	178.5	10.6	299	14	US-10-123-090A-54	Sequence 54, App1
265	178.5	10.6	299	14	US-10-127-838B-366	Sequence 366, App	338	178.5	10.6	299	14	US-10-127-847A-366	Sequence 366, App
266	178.5	10.6	299	14	US-10-127-843A-366	Sequence 366, App	339	178.5	10.6	299	14	US-10-146-727A-366	Sequence 366, App
267	178.5	10.6	299	14	US-10-127-845A-366	Sequence 366, App	340	178.5	10.6	299	14	US-10-146-728A-366	Sequence 366, App
268	178.5	10.6	299	14	US-10-127-846A-366	Sequence 366, App	341	178.5	10.6	299	14	US-10-175-590A-366	Sequence 366, App
269	178.5	10.6	299	14	US-10-127-848A-366	Sequence 366, App	342	178.5	10.6	299	14	US-10-123-089A-54	Sequence 54, App1
270	178.5	10.6	299	14	US-10-127-849A-366	Sequence 366, App	343	178.5	10.6	299	14	US-10-137-826A-366	Sequence 366, App
271	178.5	10.6	299	14	US-10-127-850A-366	Sequence 366, App	344	178.5	10.6	299	14	US-10-146-726A-366	Sequence 366, App
272	178.5	10.6	299	14	US-10-127-851A-366	Sequence 366, App	345	178.5	10.6	299	14	US-10-146-727A-366	Sequence 366, App
273	178.5	10.6	299	14	US-10-128-684A-366	Sequence 366, App	346	178.5	10.6	299	14	US-10-146-728A-366	Sequence 366, App
274	178.5	10.6	299	14	US-10-128-686A-366	Sequence 366, App	347	178.5	10.6	299	14	US-10-152-380A-366	Sequence 366, App
275	178.5	10.6	299	14	US-10-128-690A-366	Sequence 366, App	348	178.5	10.6	299	14	US-10-153-934A-366	Sequence 366, App
276	178.5	10.6	299	14	US-10-128-691A-366	Sequence 366, App	349	178.5	10.6	299	14	US-10-140-807A-366	Sequence 366, App
277	178.5	10.6	299	14	US-10-131-819A-366	Sequence 366, App	350	178.5	10.6	299	14	US-10-140-924A-366	Sequence 366, App
278	178.5	10.6	299	14	US-10-131-829A-366	Sequence 366, App	351	178.5	10.6	299	14	US-10-140-926A-366	Sequence 366, App
279	178.5	10.6	299	14	US-10-131-836A-366	Sequence 366, App	352	178.5	10.6	299	14	US-10-141-698A-366	Sequence 366, App
280	178.5	10.6	299	14	US-10-146-729A-366	Sequence 366, App	353	178.5	10.6	299	14	US-10-141-702A-366	Sequence 366, App
281	178.5	10.6	299	14	US-10-146-731A-366	Sequence 366, App	354	178.5	10.6	299	14	US-10-141-704A-366	Sequence 366, App
282	178.5	10.6	299	14	US-10-147-404A-366	Sequence 366, App	355	178.5	10.6	299	14	US-10-142-421A-366	Sequence 366, App
283	178.5	10.6	299	14	US-10-147-408A-366	Sequence 366, App	356	178.5	10.6	299	14	US-10-142-432A-366	Sequence 366, App
284	178.5	10.6	299	14	US-10-147-512A-366	Sequence 366, App	357	178.5	10.6	299	14	US-10-142-767A-366	Sequence 366, App
285	178.5	10.6	299	14	US-10-175-735A-366	Sequence 366, App	358	178.5	10.6	299	14	US-10-143-033A-366	Sequence 366, App
286	178.5	10.6	299	14	US-10-121-040A-366	Sequence 366, App	359	178.5	10.6	299	14	US-10-144-994A-366	Sequence 366, App
287	178.5	10.6	299	14	US-10-121-056A-366	Sequence 366, App	360	178.5	10.6	299	14	US-10-145-628A-366	Sequence 366, App
288	178.5	10.6	299	14	US-10-121-061A-366	Sequence 366, App	361	178.5	10.6	299	14	US-10-145-746A-366	Sequence 366, App
289	178.5	10.6	299	14	US-10-123-235A-366	Sequence 366, App	362	178.5	10.6	299	14	US-10-145-748A-366	Sequence 366, App
290	178.5	10.6	299	14	US-10-124-818A-366	Sequence 366, App	363	178.5	10.6	299	14	US-10-145-823A-366	Sequence 366, App
291	178.5	10.6	299	14	US-10-137-868A-366	Sequence 366, App	364	178.5	10.6	299	14	US-10-145-826A-366	Sequence 366, App
292	178.5	10.6	299	14	US-10-147-492A-366	Sequence 366, App	365	178.5	10.6	299	14	US-10-145-870A-366	Sequence 366, App
293	178.5	10.6	299	14	US-10-158-782A-366	Sequence 366, App	366	178.5	10.6	299	14	US-10-145-876A-366	Sequence 366, App
294	178.5	10.6	299	14	US-10-123-905A-366	Sequence 366, App	367	178.5	10.6	299	14	US-10-145-959A-366	Sequence 366, App
295	178.5	10.6	299	14	US-10-123-907A-366	Sequence 366, App	368	178.5	10.6	299	14	US-10-146-724A-366	Sequence 366, App
296	178.5	10.6	299	14	US-10-124-815A-366	Sequence 366, App	369	178.5	10.6	299	14	US-10-146-725A-366	Sequence 366, App
297	178.5	10.6	299	14	US-10-125-921A-366	Sequence 366, App	370	178.5	10.6	299	14	US-10-146-795A-366	Sequence 366, App
298	178.5	10.6	299	14	US-10-125-928A-366	Sequence 366, App	371	178.5	10.6	299	14	US-10-147-495A-366	Sequence 366, App
299	178.5	10.6	299	14	US-10-127-821A-366	Sequence 366, App	372	178.5	10.6	299	14	US-10-147-501A-366	Sequence 366, App
300	178.5	10.6	299	14	US-10-127-822A-366	Sequence 366, App	373	178.5	10.6	299	14	US-10-147-504A-366	Sequence 366, App
301	178.5	10.6	299	14	US-10-127-824A-366	Sequence 366, App	374	178.5	10.6	299	14	US-10-147-509A-366	Sequence 366, App
302	178.5	10.6	299	14	US-10-127-826A-366	Sequence 366, App	375	178.5	10.6	299	14	US-10-147-510A-366	Sequence 366, App
303	178.5	10.6	299	14	US-10-127-827A-366	Sequence 366, App	376	178.5	10.6	299	14	US-10-147-511A-366	Sequence 366, App
304	178.5	10.6	299	14	US-10-127-828A-366	Sequence 366, App	377	178.5	10.6	299	14	US-10-147-529A-366	Sequence 366, App
305	178.5	10.6	299	14	US-10-127-830A-366	Sequence 366, App	378	178.5	10.6	299	14	US-10-147-529A-366	Sequence 366, App

379	178.5	10.6	299	14	US-10-152-397-366	Sequence 366, App	452	178.5	10.6	299	14	US-10-147-483-366	Sequence 366, App
380	178.5	10.6	299	14	US-10-153-586-366	Sequence 366, App	453	178.5	10.6	299	14	US-10-147-486-366	Sequence 366, App
381	178.5	10.6	299	14	US-10-158-836-366	Sequence 366, App	454	178.5	10.6	299	14	US-10-147-487-366	Sequence 366, App
382	178.5	10.6	299	14	US-10-137-870-366	Sequence 366, App	455	178.5	10.6	299	14	US-10-147-490-366	Sequence 366, App
383	178.5	10.6	299	14	US-10-140-018-366	Sequence 366, App	456	178.5	10.6	299	14	US-10-147-494-366	Sequence 366, App
384	178.5	10.6	299	14	US-10-140-021-366	Sequence 366, App	457	178.5	10.6	299	14	US-10-147-498-366	Sequence 366, App
385	178.5	10.6	299	14	US-10-140-471-366	Sequence 366, App	458	178.5	10.6	299	14	US-10-147-514-366	Sequence 366, App
386	178.5	10.6	299	14	US-10-140-922-366	Sequence 366, App	459	178.5	10.6	299	14	US-10-147-524-366	Sequence 366, App
387	178.5	10.6	299	14	US-10-145-631-366	Sequence 366, App	460	178.5	10.6	299	14	US-10-152-379-366	Sequence 366, App
388	178.5	10.6	299	14	US-10-145-633-366	Sequence 366, App	461	178.5	10.6	299	14	US-10-152-394-366	Sequence 366, App
389	178.5	10.6	299	14	US-10-158-783-366	Sequence 366, App	462	178.5	10.6	299	14	US-10-152-406-366	Sequence 366, App
390	178.5	10.6	299	14	US-10-140-274-366	Sequence 366, App	463	178.5	10.6	299	14	US-10-156-847-366	Sequence 366, App
391	178.5	10.6	299	14	US-10-140-019-366	Sequence 366, App	464	178.5	10.6	299	14	US-10-157-778-366	Sequence 366, App
392	178.5	10.6	299	14	US-10-140-022-366	Sequence 366, App	465	178.5	10.6	299	14	US-10-157-799-366	Sequence 366, App
393	178.5	10.6	299	14	US-10-140-861-366	Sequence 366, App	466	178.5	10.6	299	14	US-10-160-504-366	Sequence 366, App
394	178.5	10.6	299	14	US-10-140-862-366	Sequence 366, App	467	178.5	10.6	299	14	US-10-160-504-366	Sequence 366, App
395	178.5	10.6	299	14	US-10-141-697-366	Sequence 366, App	468	178.5	10.6	299	14	US-10-165-542-1	Sequence 366, App
396	178.5	10.6	299	14	US-10-141-703-366	Sequence 366, App	469	178.5	10.6	299	14	US-10-147-520-366	Sequence 366, App
397	178.5	10.6	299	14	US-10-141-703-366	Sequence 366, App	470	178.5	10.6	299	14	US-10-157-781-366	Sequence 366, App
398	178.5	10.6	299	14	US-10-141-753-366	Sequence 366, App	471	178.5	10.6	299	14	US-10-176-989-366	Sequence 366, App
399	178.5	10.6	299	14	US-10-142-418-366	Sequence 366, App	472	178.5	10.6	299	14	US-10-176-989-366	Sequence 366, App
400	178.5	10.6	299	14	US-10-142-418-366	Sequence 366, App	473	178.5	10.6	299	14	US-10-147-491-366	Sequence 366, App
401	178.5	10.6	299	14	US-10-142-420-366	Sequence 366, App	474	178.5	10.6	299	14	US-10-152-378-366	Sequence 366, App
402	178.5	10.6	299	14	US-10-142-422-366	Sequence 366, App	475	178.5	10.6	299	14	US-10-152-382-366	Sequence 366, App
403	178.5	10.6	299	14	US-10-142-427-366	Sequence 366, App	476	178.5	10.6	299	14	US-10-152-383-366	Sequence 366, App
404	178.5	10.6	299	14	US-10-142-760-366	Sequence 366, App	477	178.5	10.6	299	14	US-10-157-784-366	Sequence 366, App
405	178.5	10.6	299	14	US-10-145-821-366	Sequence 366, App	478	178.5	10.6	299	14	US-10-152-387-366	Sequence 366, App
406	178.5	10.6	299	14	US-10-152-531-366	Sequence 366, App	479	178.5	10.6	299	14	US-10-152-389-366	Sequence 366, App
407	178.5	10.6	299	14	US-10-127-840X-366	Sequence 366, App	480	178.5	10.6	299	14	US-10-152-390-366	Sequence 366, App
408	178.5	10.6	299	14	US-10-142-424-366	Sequence 366, App	481	178.5	10.6	299	14	US-10-152-392-366	Sequence 366, App
409	178.5	10.6	299	14	US-10-142-761-366	Sequence 366, App	482	178.5	10.6	299	14	US-10-153-756-366	Sequence 366, App
410	178.5	10.6	299	14	US-10-142-763-366	Sequence 366, App	483	178.5	10.6	299	14	US-10-157-784-366	Sequence 366, App
411	178.5	10.6	299	14	US-10-142-765-366	Sequence 366, App	484	178.5	10.6	299	14	US-10-157-797-366	Sequence 366, App
412	178.5	10.6	299	14	US-10-142-887-366	Sequence 366, App	485	178.5	10.6	299	14	US-10-158-491-366	Sequence 366, App
413	178.5	10.6	299	14	US-10-142-888-366	Sequence 366, App	486	178.5	10.6	299	14	US-10-299-976-119	Sequence 366, App
414	178.5	10.6	299	14	US-10-143-034-366	Sequence 366, App	487	178.5	10.6	299	14	US-10-066-203-91	Sequence 366, App
415	178.5	10.6	299	14	US-10-143-116-366	Sequence 366, App	488	178.5	10.6	299	14	US-10-142-762-366	Sequence 366, App
416	178.5	10.6	299	14	US-10-144-957-366	Sequence 366, App	489	178.5	10.6	299	14	US-10-142-764-366	Sequence 366, App
417	178.5	10.6	299	14	US-10-144-959-366	Sequence 366, App	490	178.5	10.6	299	14	US-10-142-766-366	Sequence 366, App
418	178.5	10.6	299	14	US-10-145-015-366	Sequence 366, App	491	178.5	10.6	299	14	US-10-145-625-366	Sequence 366, App
419	178.5	10.6	299	14	US-10-145-090-366	Sequence 366, App	492	178.5	10.6	299	14	US-10-145-627-366	Sequence 366, App
420	178.5	10.6	299	14	US-10-145-091-366	Sequence 366, App	493	178.5	10.6	299	14	US-10-145-960-366	Sequence 366, App
421	178.5	10.6	299	14	US-10-145-629-366	Sequence 366, App	494	178.5	10.6	299	14	US-10-145-962-366	Sequence 366, App
422	178.5	10.6	299	14	US-10-145-630-366	Sequence 366, App	495	178.5	10.6	299	14	US-10-146-789-366	Sequence 366, App
423	178.5	10.6	299	14	US-10-145-747-366	Sequence 366, App	496	178.5	10.6	299	14	US-10-147-483-366	Sequence 366, App
424	178.5	10.6	299	14	US-10-145-752-366	Sequence 366, App	497	178.5	10.6	299	14	US-10-147-496-366	Sequence 366, App
425	178.5	10.6	299	14	US-10-145-754-366	Sequence 366, App	498	178.5	10.6	299	14	US-10-147-505-366	Sequence 366, App
426	178.5	10.6	299	14	US-10-145-755-366	Sequence 366, App	499	178.5	10.6	299	14	US-10-147-516-366	Sequence 366, App
427	178.5	10.6	299	14	US-10-145-818-366	Sequence 366, App	500	178.5	10.6	299	14	US-10-152-398-366	Sequence 366, App
428	178.5	10.6	299	14	US-10-145-820-366	Sequence 366, App	501	178.5	10.6	299	14	US-10-139-980-366	Sequence 366, App
429	178.5	10.6	299	14	US-10-145-872-366	Sequence 366, App	502	178.5	10.6	299	14	US-10-129-937-119	Sequence 366, App
430	178.5	10.6	299	14	US-10-145-873-366	Sequence 366, App	503	178.5	10.6	299	14	US-10-145-973-366	Sequence 366, App
431	178.5	10.6	299	14	US-10-147-481-366	Sequence 366, App	504	178.5	10.6	299	14	US-10-152-373-366	Sequence 366, App
432	178.5	10.6	299	14	US-10-147-482-366	Sequence 366, App	505	178.5	10.6	299	14	US-10-1223-081-34	Sequence 366, App
433	178.5	10.6	299	14	US-10-147-522-366	Sequence 366, App	506	178.5	10.6	299	14	US-10-121-044-366	Sequence 366, App
434	178.5	10.6	299	14	US-10-147-503-366	Sequence 366, App	507	178.5	10.6	299	14	US-10-121-055-366	Sequence 366, App
435	178.5	10.6	299	14	US-10-152-401-366	Sequence 366, App	508	178.5	10.6	299	14	US-10-123-157-366	Sequence 366, App
436	178.5	10.6	299	14	US-10-157-783-366	Sequence 366, App	509	178.5	10.6	299	14	US-10-121-058-366	Sequence 366, App
437	178.5	10.6	299	14	US-10-158-792-366	Sequence 366, App	510	178.5	10.6	299	14	US-10-121-059-366	Sequence 366, App
438	178.5	10.6	299	14	US-10-158-462-366	Sequence 366, App	511	178.5	10.6	299	14	US-10-121-060-366	Sequence 366, App
439	178.5	10.6	299	14	US-10-143-035-366	Sequence 366, App	512	178.5	10.6	299	14	US-10-123-109-366	Sequence 366, App
440	178.5	10.6	299	14	US-10-145-751-366	Sequence 366, App	513	178.5	10.6	299	14	US-10-123-154-366	Sequence 366, App
441	178.5	10.6	299	14	US-10-145-822-366	Sequence 366, App	514	178.5	10.6	299	14	US-10-123-157-366	Sequence 366, App
442	178.5	10.6	299	14	US-10-145-824-366	Sequence 366, App	515	178.5	10.6	299	14	US-10-123-906-366	Sequence 366, App
443	178.5	10.6	299	14	US-10-145-827-366	Sequence 366, App	516	178.5	10.6	299	14	US-10-124-814-366	Sequence 366, App
444	178.5	10.6	299	14	US-10-145-869-366	Sequence 366, App	517	178.5	10.6	299	14	US-10-124-816-366	Sequence 366, App
445	178.5	10.6	299	14	US-10-145-875-366	Sequence 366, App	518	178.5	10.6	299	14	US-10-124-820-366	Sequence 366, App
446	178.5	10.6	299	14	US-10-145-877-366	Sequence 366, App	519	178.5	10.6	299	14	US-10-125-704-366	Sequence 366, App
447	178.5	10.6	299	14	US-10-145-958-366	Sequence 366, App	520	178.5	10.6	299	14	US-10-125-927-366	Sequence 366, App
448	178.5	10.6	299	14	US-10-146-787-366	Sequence 366, App	521	178.5	10.6	299	14	US-10-1223-082-54	Sequence 366, App
449	178.5	10.6	299	14	US-10-146-790-366	Sequence 366, App	522	178.5	10.6	299	14	US-10-142-889-366	Sequence 366, App
450	178.5	10.6	299	14	US-10-146-793-366	Sequence 366, App	523	178.5	10.6	299	14	US-10-145-874-366	Sequence 366, App
451	178.5	10.6	299	14	US-10-147-480-366	Sequence 366, App	524	178.5	10.6	299	14	US-10-147-497-366	Sequence 366, App

525	178.5	10.6	299	14	US-10-152-371-366	Sequence 366, App	598	178.5	10.6	299	14	US-10-147-489-366	Sequence 366, App
526	178.5	10.6	299	14	US-10-152-374-366	Sequence 366, App	599	178.5	10.6	299	14	US-10-147-507-366	Sequence 366, App
527	178.5	10.6	299	14	US-10-152-375-366	Sequence 366, App	600	178.5	10.6	299	14	US-10-147-533-366	Sequence 366, App
528	178.5	10.6	299	14	US-10-152-377-366	Sequence 366, App	601	178.5	10.6	299	14	US-10-147-537-366	Sequence 366, App
529	178.5	10.6	299	14	US-10-152-386-366	Sequence 366, App	602	178.5	10.6	299	14	US-10-152-376-366	Sequence 366, App
530	178.5	10.6	299	14	US-10-152-391-366	Sequence 366, App	603	178.5	10.6	299	14	US-10-152-381-366	Sequence 366, App
531	178.5	10.6	299	14	US-10-152-399-366	Sequence 366, App	604	178.5	10.6	299	14	US-10-152-400-366	Sequence 366, App
532	178.5	10.6	299	14	US-10-156-848-366	Sequence 366, App	605	178.5	10.6	299	14	US-10-153-588-366	Sequence 366, App
533	178.5	10.6	299	14	US-10-157-785-366	Sequence 366, App	606	178.5	10.6	299	14	US-10-157-780-366	Sequence 366, App
534	178.5	10.6	299	14	US-10-157-794-366	Sequence 366, App	607	178.5	10.6	299	14	US-10-157-800-366	Sequence 366, App
535	178.5	10.6	299	14	US-10-157-796-366	Sequence 366, App	608	178.5	10.6	299	14	US-10-157-801-366	Sequence 366, App
536	178.5	10.6	299	14	US-10-160-500-366	Sequence 366, App	609	178.5	10.6	299	14	US-10-157-802-366	Sequence 366, App
537	178.5	10.6	299	14	US-10-121-046-366	Sequence 366, App	610	178.5	10.6	299	14	US-10-158-783-366	Sequence 366, App
538	178.5	10.6	299	14	US-10-123-156-366	Sequence 366, App	611	178.5	10.6	299	14	US-10-158-789-366	Sequence 366, App
539	178.5	10.6	299	14	US-10-123-214-366	Sequence 366, App	612	178.5	10.6	299	14	US-10-192-011-366	Sequence 366, App
540	178.5	10.6	299	14	US-10-125-805-366	Sequence 366, App	613	178.5	10.6	299	14	US-10-139-963-366	Sequence 366, App
541	178.5	10.6	299	14	US-10-124-821-366	Sequence 366, App	614	178.5	10.6	299	14	US-10-140-020-366	Sequence 366, App
542	178.5	10.6	299	14	US-10-152-385-366	Sequence 366, App	615	178.5	10.6	299	14	US-10-140-023-366	Sequence 366, App
543	178.5	10.6	299	14	US-10-152-393-366	Sequence 366, App	616	178.5	10.6	299	14	US-10-140-809-366	Sequence 366, App
544	178.5	10.6	299	14	US-10-152-396-366	Sequence 366, App	617	178.5	10.6	299	14	US-10-140-865-366	Sequence 366, App
545	178.5	10.6	299	14	US-10-153-552-366	Sequence 366, App	618	178.5	10.6	299	14	US-10-141-701-366	Sequence 366, App
546	178.5	10.6	299	14	US-10-153-840-366	Sequence 366, App	619	178.5	10.6	299	14	US-10-141-753-366	Sequence 366, App
547	178.5	10.6	299	14	US-10-156-841-366	Sequence 366, App	620	178.5	10.6	299	14	US-10-141-760-366	Sequence 366, App
548	178.5	10.6	299	14	US-10-156-842-366	Sequence 366, App	621	178.5	10.6	299	14	US-10-142-425-366	Sequence 366, App
549	178.5	10.6	299	14	US-10-156-844-366	Sequence 366, App	622	178.5	10.6	299	14	US-10-142-430-366	Sequence 366, App
550	178.5	10.6	299	14	US-10-156-845-366	Sequence 366, App	623	178.5	10.6	299	14	US-10-143-113-366	Sequence 366, App
551	178.5	10.6	299	14	US-10-156-846-366	Sequence 366, App	624	178.5	10.6	299	14	US-10-146-730-366	Sequence 366, App
552	178.5	10.6	299	14	US-10-121-048-366	Sequence 366, App	625	178.5	10.6	299	14	US-10-146-792-366	Sequence 366, App
553	178.5	10.6	299	14	US-10-121-052-366	Sequence 366, App	626	178.5	10.6	299	14	US-10-158-791-366	Sequence 366, App
554	178.5	10.6	299	14	US-10-121-053-366	Sequence 366, App	627	178.5	10.6	299	14	US-10-156-843-366	Sequence 366, App
555	178.5	10.6	299	14	US-10-121-054-366	Sequence 366, App	628	178.5	10.6	299	14	US-10-157-786-366	Sequence 366, App
556	178.5	10.6	299	14	US-10-121-063-366	Sequence 366, App	629	178.5	10.6	299	14	US-10-152-405-366	Sequence 366, App
557	178.5	10.6	299	14	US-10-123-212-366	Sequence 366, App	630	178.5	10.6	299	14	US-10-1298-993-119	Sequence 366, App
558	178.5	10.6	299	14	US-10-123-213-366	Sequence 366, App	631	178.5	10.6	299	14	US-10-147-528-366	Sequence 366, App
559	178.5	10.6	299	14	US-10-123-291-366	Sequence 366, App	632	178.5	10.6	299	14	US-10-1305-654-54	Sequence 366, App
560	178.5	10.6	299	14	US-10-123-322-366	Sequence 366, App	633	178.5	10.6	299	14	US-10-148-923-119	Sequence 366, App
561	178.5	10.6	299	14	US-10-123-322-366	Sequence 366, App	634	178.5	10.6	299	14	US-10-291-265-275	Sequence 366, App
562	178.5	10.6	299	14	US-10-123-911-366	Sequence 366, App	635	178.5	10.6	299	14	US-10-291-265-747	Sequence 366, App
563	178.5	10.6	299	14	US-10-124-823-366	Sequence 366, App	636	178.5	10.6	299	14	US-10-291-265-748	Sequence 366, App
564	178.5	10.6	299	14	US-10-125-931-366	Sequence 366, App	637	178.5	10.6	299	15	US-10-449-656-119	Sequence 366, App
565	178.5	10.6	299	14	US-10-125-932-366	Sequence 366, App	638	178.5	10.6	299	15	US-10-448-713-119	Sequence 366, App
566	178.5	10.6	299	14	US-10-127-852-366	Sequence 366, App	639	178.5	10.6	299	15	US-10-264-237-2666	Sequence 366, App
567	178.5	10.6	299	14	US-10-127-852-366	Sequence 366, App	640	178.5	10.6	299	15	US-10-128-692A-366	Sequence 366, App
568	178.5	10.6	299	14	US-10-128-685A-366	Sequence 366, App	641	178.5	10.6	299	15	US-10-140-927-366	Sequence 366, App
569	178.5	10.6	299	14	US-10-131-820A-366	Sequence 366, App	642	178.5	10.6	299	15	US-10-425-447-119	Sequence 366, App
570	178.5	10.6	299	14	US-10-142-886-366	Sequence 366, App	643	178.5	10.6	299	15	US-10-147-493-366	Sequence 366, App
571	178.5	10.6	299	14	US-10-146-728-366	Sequence 366, App	644	178.5	10.6	299	15	US-10-145-127-366	Sequence 366, App
572	178.5	10.6	299	14	US-10-146-786-366	Sequence 366, App	645	178.5	10.6	299	15	US-10-160-503-366	Sequence 366, App
573	178.5	10.6	299	14	US-10-147-499-366	Sequence 366, App	646	178.5	10.6	299	15	US-10-143-118-366	Sequence 366, App
574	178.5	10.6	299	14	US-10-157-798-366	Sequence 366, App	647	178.5	10.6	299	15	US-10-144-993-366	Sequence 366, App
575	178.5	10.6	299	14	US-10-123-913-366	Sequence 366, App	648	178.5	10.6	299	15	US-10-158-787-366	Sequence 366, App
576	178.5	10.6	299	14	US-10-140-473-366	Sequence 366, App	649	178.5	10.6	299	15	US-10-081-056-54	Sequence 366, App
577	178.5	10.6	299	14	US-10-140-806-366	Sequence 366, App	650	178.5	10.6	299	15	US-10-140-024-366	Sequence 366, App
578	178.5	10.6	299	14	US-10-140-810-366	Sequence 366, App	651	178.5	10.6	299	15	US-10-147-536-366	Sequence 366, App
579	178.5	10.6	299	14	US-10-140-863-366	Sequence 366, App	652	178.5	10.6	299	15	US-10-601-953-887	Sequence 366, App
580	178.5	10.6	299	14	US-10-141-699-366	Sequence 366, App	653	178.5	10.6	299	16	US-10-633-008-1	Sequence 366, App
581	178.5	10.6	299	14	US-10-141-703-366	Sequence 366, App	654	178.5	10.6	299	16	US-10-152-372-366	Sequence 366, App
582	178.5	10.6	299	14	US-10-141-706-366	Sequence 366, App	655	178.5	10.6	299	16	US-10-215-371-119	Sequence 366, App
583	178.5	10.6	299	14	US-10-141-707-366	Sequence 366, App	656	178.5	10.6	299	16	US-10-785-220-1	Sequence 366, App
584	178.5	10.6	299	14	US-10-141-762-366	Sequence 366, App	657	178.5	10.6	299	16	US-10-785-221-1	Sequence 366, App
585	178.5	10.6	299	14	US-10-142-428-366	Sequence 366, App	658	178.5	10.6	299	16	US-10-785-433-1	Sequence 366, App
586	178.5	10.6	299	14	US-10-142-429-366	Sequence 366, App	659	178.5	10.6	299	16	US-10-771-187-119	Sequence 366, App
587	178.5	10.6	299	14	US-10-142-884-366	Sequence 366, App	660	178.5	10.6	299	17	US-10-123-793-366	Sequence 366, App
588	178.5	10.6	299	14	US-10-143-027-366	Sequence 366, App	661	178.5	10.6	299	17	US-10-145-626-366	Sequence 366, App
589	178.5	10.6	299	14	US-10-143-115-366	Sequence 366, App	662	178.5	10.6	299	17	US-10-145-819-366	Sequence 366, App
590	178.5	10.6	299	14	US-10-144-956-366	Sequence 366, App	663	178.5	10.6	299	17	US-10-145-825-366	Sequence 366, App
591	178.5	10.6	299	14	US-10-144-958-366	Sequence 366, App	664	178.5	10.6	299	17	US-10-147-513-366	Sequence 366, App
592	178.5	10.6	299	14	US-10-145-632-366	Sequence 366, App	665	178.5	10.6	299	17	US-10-147-518-366	Sequence 366, App
593	178.5	10.6	299	14	US-10-145-749-366	Sequence 366, App	666	178.5	10.6	299	17	US-10-167-374-1	Sequence 366, App
594	178.5	10.6	299	14	US-10-145-753-366	Sequence 366, App	667	178.5	10.6	299	17	US-10-1785-607-1	Sequence 366, App
595	178.5	10.6	299	14	US-10-145-871-366	Sequence 366, App	668	178.5	10.6	299	17	US-10-145-961-366	Sequence 366, App
596	178.5	10.6	299	14	US-10-145-878-366	Sequence 366, App	669	178.5	10.6	299	17	US-10-785-351-3	Sequence 366, App
597	178.5	10.6	299	14	US-10-146-794-366	Sequence 366, App	670	178.5	10.6	299	17	US-10-147-488-366	Sequence 366, App

671	178.5	10.6	239	17	US-10-147-531-366	Sequence 366, App	744	158	9.4	352	9	US-09-989-735-505	Sequence 505, App
672	178.5	10.6	320	17	US-10-128-558-376	Sequence 376, App	745	158	9.4	352	9	US-09-990-444-505	Sequence 505, App
673	178.5	10.6	326	17	US-10-128-558-193	Sequence 193, App	746	158	9.4	352	9	US-09-991-181-505	Sequence 505, App
674	177	10.5	339	9	US-09-981-353-65	Sequence 65, App1	747	158	9.4	352	9	US-09-989-730-505	Sequence 505, App
675	177	10.5	339	9	US-09-953-499-6	Sequence 6, App1	748	158	9.4	352	9	US-09-990-437-505	Sequence 505, App
676	177	10.5	339	14	US-10-265-542-6	Sequence 6, App1	749	158	9.4	352	9	US-09-993-686-505	Sequence 505, App
677	177	10.5	339	14	US-10-295-027-1165	Sequence 1165, App	750	158	9.4	352	10	US-09-989-734-505	Sequence 505, App
678	177	10.5	319	16	US-10-633-008-6	Sequence 6, App1	751	158	9.4	352	10	US-09-997-653-505	Sequence 505, App
679	177	10.5	319	16	US-10-785-220-6	Sequence 6, App1	752	158	9.4	352	10	US-09-989-724-505	Sequence 505, App
680	177	10.5	319	16	US-10-785-221-6	Sequence 6, App1	753	158	9.4	352	10	US-09-989-728-505	Sequence 505, App
681	177	10.5	319	16	US-10-785-433-6	Sequence 6, App1	754	158	9.4	352	10	US-09-990-441-505	Sequence 505, App
682	177	10.5	319	17	US-10-767-374-6	Sequence 6, App1	755	158	9.4	352	10	US-09-993-667-505	Sequence 505, App
683	177	10.5	319	17	US-10-785-607-6	Sequence 6, App1	756	158	9.4	352	10	US-09-997-428-505	Sequence 505, App
684	177	10.5	336	15	US-10-363-616-318	Sequence 318, App	757	158	9.4	352	10	US-09-997-666-505	Sequence 505, App
685	176	10.4	268	14	US-10-265-542-24	Sequence 24, App1	758	158	9.4	352	10	US-09-990-438-505	Sequence 505, App
686	176	10.4	268	16	US-10-633-008-24	Sequence 24, App1	759	158	9.4	352	10	US-09-990-562-505	Sequence 505, App
687	176	10.4	270	9	US-09-953-499-24	Sequence 24, App1	760	158	9.4	352	10	US-09-990-711-505	Sequence 505, App
688	176	10.4	270	16	US-10-785-220-24	Sequence 24, App1	761	158	9.4	352	10	US-09-989-726-505	Sequence 505, App
689	176	10.4	270	16	US-10-785-221-24	Sequence 24, App1	762	158	9.4	352	10	US-09-998-156-505	Sequence 505, App
690	176	10.4	270	16	US-10-785-433-24	Sequence 24, App1	763	158	9.4	352	10	US-09-990-437-505	Sequence 505, App
691	176	10.4	270	17	US-10-767-374-24	Sequence 24, App1	764	158	9.4	352	10	US-09-991-157-505	Sequence 505, App
692	176	10.4	270	17	US-10-785-607-24	Sequence 24, App1	765	158	9.4	352	10	US-09-997-514-505	Sequence 505, App
693	176	10.4	273	9	US-09-953-499-26	Sequence 26, App1	766	158	9.4	352	10	US-09-997-573-505	Sequence 505, App
694	176	10.4	273	14	US-10-265-542-26	Sequence 26, App1	767	158	9.4	352	10	US-09-991-172-505	Sequence 505, App
695	176	10.4	273	16	US-10-633-008-26	Sequence 26, App1	768	158	9.4	352	10	US-09-990-726-505	Sequence 505, App
696	176	10.4	273	16	US-10-785-220-26	Sequence 26, App1	769	158	9.4	352	10	US-09-997-559-505	Sequence 505, App
697	176	10.4	273	16	US-10-785-221-26	Sequence 26, App1	770	158	9.4	352	10	US-09-997-601-505	Sequence 505, App
698	176	10.4	273	16	US-10-785-433-26	Sequence 26, App1	771	158	9.4	352	10	US-09-990-443-505	Sequence 505, App
699	176	10.4	273	17	US-10-767-374-26	Sequence 26, App1	772	158	9.4	352	10	US-09-991-854-505	Sequence 505, App
700	176	10.4	273	17	US-10-785-607-26	Sequence 26, App1	773	158	9.4	352	10	US-09-997-628-505	Sequence 505, App
701	172.5	10.2	316	17	US-10-785-351-13	Sequence 13, App1	774	158	9.4	352	10	US-09-997-683-505	Sequence 505, App
702	171	10.1	47	17	US-10-425-115-29346	Sequence 29346, App	775	158	9.4	352	10	US-09-989-729A-505	Sequence 505, App
703	169.5	10.0	260	9	US-09-953-499-23	Sequence 23, App1	776	158	9.4	352	10	US-09-997-349-505	Sequence 505, App
704	169.5	10.0	260	14	US-10-265-542-23	Sequence 23, App1	777	158	9.4	352	10	US-09-997-440-505	Sequence 505, App
705	169.5	10.0	260	16	US-10-633-008-23	Sequence 23, App1	778	158	9.4	352	10	US-09-990-440-505	Sequence 505, App
706	169.5	10.0	260	16	US-10-785-220-23	Sequence 23, App1	779	158	9.4	352	10	US-09-997-857-505	Sequence 505, App
707	169.5	10.0	260	16	US-10-785-221-23	Sequence 23, App1	780	158	9.4	352	10	US-09-993-469-505	Sequence 505, App
708	169.5	10.0	260	16	US-10-785-433-23	Sequence 23, App1	781	158	9.4	352	10	US-09-997-542-505	Sequence 505, App
709	169.5	10.0	260	17	US-10-767-374-23	Sequence 23, App1	782	158	9.4	352	10	US-09-993-748-505	Sequence 505, App
710	169.5	10.0	260	17	US-10-785-607-23	Sequence 23, App1	783	158	9.4	352	10	US-09-990-439-505	Sequence 505, App
711	169.5	10.0	263	9	US-09-953-499-25	Sequence 25, App1	784	158	9.4	352	10	US-09-990-427-505	Sequence 505, App
712	169.5	10.0	263	14	US-10-265-542-25	Sequence 25, App1	785	158	9.4	352	10	US-09-989-338-505	Sequence 505, App
713	169.5	10.0	263	16	US-10-633-008-25	Sequence 25, App1	786	158	9.4	352	10	US-09-993-583-505	Sequence 505, App
714	169.5	10.0	263	16	US-10-785-220-25	Sequence 25, App1	787	158	9.4	352	10	US-09-994-592-505	Sequence 505, App
715	169.5	10.0	263	16	US-10-785-221-25	Sequence 25, App1	788	158	9.4	352	10	US-09-997-521-505	Sequence 505, App
716	169.5	10.0	263	16	US-10-785-433-25	Sequence 25, App1	789	158	9.4	352	10	US-09-997-333-505	Sequence 505, App
717	169.5	10.0	263	17	US-10-767-374-25	Sequence 25, App1	790	158	9.4	352	10	US-09-997-384-505	Sequence 505, App
718	169.5	10.0	263	17	US-10-785-607-25	Sequence 25, App1	791	158	9.4	352	10	US-09-998-041-505	Sequence 505, App
719	167	9.9	300	9	US-09-953-499-10	Sequence 10, App1	792	158	9.4	352	10	US-09-997-585-505	Sequence 505, App
720	167	9.9	300	14	US-10-265-542-10	Sequence 10, App1	793	158	9.4	352	10	US-09-997-614-505	Sequence 505, App
721	167	9.9	300	16	US-10-633-008-10	Sequence 10, App1	794	158	9.4	352	10	US-09-989-862-505	Sequence 505, App
722	167	9.9	300	16	US-10-785-220-10	Sequence 10, App1	795	158	9.4	352	10	US-09-997-529-505	Sequence 505, App
723	167	9.9	300	16	US-10-785-221-10	Sequence 10, App1	796	158	9.4	352	10	US-09-989-725-505	Sequence 505, App
724	167	9.9	300	16	US-10-785-433-10	Sequence 10, App1	797	158	9.4	352	10	US-09-991-150-505	Sequence 505, App
725	167	9.9	300	17	US-10-767-374-10	Sequence 10, App1	798	158	9.4	352	10	US-09-997-641-505	Sequence 505, App
726	167	9.9	300	17	US-10-785-607-10	Sequence 10, App1	799	158	9.4	352	10	US-09-989-733-505	Sequence 505, App
727	167	9.9	300	17	US-10-785-351-12	Sequence 12, App1	800	158	9.4	352	10	US-09-992-643-505	Sequence 505, App
728	166	9.8	365	9	US-09-899-634A-4	Sequence 4, App1	801	158	9.4	352	13	US-10-053-107-10	Sequence 10, App1
729	163.5	9.7	261	9	US-09-899-634A-2	Sequence 2, App1	802	158	9.4	352	14	US-10-227-884-216	Sequence 216, App
730	158	9.4	352	9	US-09-989-722-505	Sequence 505, App	803	158	9.4	352	14	US-10-230-163-216	Sequence 216, App
731	158	9.4	352	9	US-09-989-723-505	Sequence 505, App	804	158	9.4	352	14	US-10-230-338-216	Sequence 216, App
732	158	9.4	352	9	US-09-989-727-505	Sequence 505, App	805	158	9.4	352	14	US-10-218-631-216	Sequence 216, App
733	158	9.4	352	9	US-09-989-729-505	Sequence 505, App	806	158	9.4	352	14	US-10-230-414-216	Sequence 216, App
734	158	9.4	352	9	US-09-989-731-505	Sequence 505, App	807	158	9.4	352	14	US-10-213-145-10	Sequence 10, App1
735	158	9.4	352	9	US-09-989-732-505	Sequence 505, App	808	158	9.4	352	14	US-10-233-224-216	Sequence 216, App
736	158	9.4	352	9	US-09-991-073-505	Sequence 505, App	809	158	9.4	352	14	US-10-216-159A-216	Sequence 216, App
737	158	9.4	352	9	US-09-990-442-505	Sequence 505, App	810	158	9.4	352	14	US-10-218-849-216	Sequence 216, App
738	158	9.4	352	9	US-09-991-163-505	Sequence 505, App	811	158	9.4	352	14	US-10-227-873-216	Sequence 216, App
739	158	9.4	352	9	US-09-993-604-505	Sequence 505, App	812	158	9.4	352	14	US-10-227-883-216	Sequence 216, App
740	158	9.4	352	9	US-09-990-456-505	Sequence 505, App	813	158	9.4	352	14	US-10-219-076-216	Sequence 216, App
741	158	9.4	352	9	US-09-989-721-505	Sequence 505, App	814	158	9.4	352	14	US-10-230-434-216	Sequence 216, App
742	158	9.4	352	9	US-09-992-598-505	Sequence 505, App	815	158	9.4	352	14	US-10-219-199-10	Sequence 10, App1
743	158	9.4	352	9	US-09-989-293A-505	Sequence 505, App	816	158	9.4	352	14	US-10-219-003-216	Sequence 216, App

817	158	352	14	US-10-219-075-216	Sequence 216, App	890	158	9.4	352	14	US-10-216-163-216	Sequence 216, App
818	158	352	14	US-10-219-464-216	Sequence 216, App	891	158	9.4	352	14	US-10-223-081-280	Sequence 280, App
819	158	352	14	US-10-219-466-216	Sequence 216, App	892	158	9.4	352	14	US-10-218-765-216	Sequence 216, App
820	158	352	14	US-10-219-479-216	Sequence 216, App	893	158	9.4	352	14	US-10-219-063-216	Sequence 216, App
821	158	352	14	US-10-219-481-216	Sequence 216, App	894	158	9.4	352	14	US-10-219-066-216	Sequence 216, App
822	158	352	14	US-10-230-260-216	Sequence 216, App	895	158	9.4	352	14	US-10-219-067-216	Sequence 216, App
823	158	352	14	US-10-232-231-216	Sequence 216, App	896	158	9.4	352	14	US-10-219-068-216	Sequence 216, App
824	158	352	14	US-10-232-233-216	Sequence 216, App	897	158	9.4	352	14	US-10-219-069-216	Sequence 216, App
825	158	352	14	US-10-216-165-216	Sequence 216, App	898	158	9.4	352	14	US-10-219-072-216	Sequence 216, App
826	158	352	14	US-10-218-956-216	Sequence 216, App	899	158	9.4	352	14	US-10-219-475-216	Sequence 216, App
827	158	352	14	US-10-219-468-216	Sequence 216, App	900	158	9.4	352	14	US-10-219-483-216	Sequence 216, App
828	158	352	14	US-10-219-478-216	Sequence 216, App	901	158	9.4	352	14	US-10-219-525-216	Sequence 216, App
829	158	352	14	US-10-219-536-216	Sequence 216, App	902	158	9.4	352	14	US-10-219-526-216	Sequence 216, App
830	158	352	14	US-10-233-205-216	Sequence 216, App	903	158	9.4	352	14	US-10-219-530-216	Sequence 216, App
831	158	352	14	US-10-219-072-216	Sequence 216, App	904	158	9.4	352	14	US-10-219-533-216	Sequence 216, App
832	158	352	14	US-10-219-470-216	Sequence 216, App	905	158	9.4	352	14	US-10-219-531-216	Sequence 216, App
833	158	352	14	US-10-219-474-216	Sequence 216, App	906	158	9.4	352	14	US-10-219-533-216	Sequence 216, App
834	158	352	14	US-10-219-524-216	Sequence 216, App	907	158	9.4	352	14	US-10-219-533-216	Sequence 216, App
835	158	352	14	US-10-219-528-216	Sequence 216, App	908	158	9.4	352	14	US-10-230-437-216	Sequence 216, App
836	158	352	14	US-10-227-880-216	Sequence 216, App	909	158	9.4	352	14	US-10-232-228-216	Sequence 216, App
837	158	352	14	US-10-227-881-216	Sequence 216, App	910	158	9.4	352	14	US-10-223-082-280	Sequence 280, App
838	158	352	14	US-10-227-882-216	Sequence 216, App	911	158	9.4	352	14	US-10-219-538-505	Sequence 505, App
839	158	352	14	US-10-230-436-216	Sequence 216, App	912	158	9.4	352	14	US-10-305-654-280	Sequence 280, App
840	158	352	14	US-10-232-223-216	Sequence 216, App	913	158	9.4	352	15	US-10-232-226-216	Sequence 216, App
841	158	352	14	US-10-232-225-216	Sequence 216, App	914	158	9.4	352	15	US-10-230-130-216	Sequence 216, App
842	158	352	14	US-10-232-227-216	Sequence 216, App	915	158	9.4	352	15	US-10-081-056-280	Sequence 280, App
843	158	352	14	US-10-232-229-216	Sequence 216, App	916	158	9.4	352	15	US-10-219-535-216	Sequence 216, App
844	158	352	14	US-10-232-234-216	Sequence 216, App	917	158	9.4	352	15	US-10-232-230-216	Sequence 216, App
845	158	352	14	US-10-219-060-216	Sequence 216, App	918	158	9.4	352	15	US-10-232-230-216	Sequence 216, App
846	158	352	14	US-10-223-085-280	Sequence 280, App	919	158	9.4	352	17	US-10-219-480-216	Sequence 216, App
847	158	352	14	US-10-216-162-216	Sequence 216, App	920	158	9.4	355	9	US-09-971-798-2	Sequence 2, App1
848	158	352	14	US-10-216-162-216	Sequence 216, App	921	158	9.4	355	14	US-10-176-847-78	Sequence 78, App1
849	158	352	14	US-10-216-164-216	Sequence 216, App	922	158	9.4	355	14	US-10-114-153-12	Sequence 12, App1
850	158	352	14	US-10-216-167-216	Sequence 216, App	923	157	9.3	353	9	US-09-971-798-31	Sequence 31, App1
851	158	352	14	US-10-216-168-216	Sequence 216, App	924	157	9.3	353	9	US-09-971-798-27	Sequence 27, App1
852	158	352	14	US-10-219-065-216	Sequence 216, App	925	153.5	9.1	353	9	US-09-796-828-52	Sequence 52, App1
853	158	352	14	US-10-219-071-216	Sequence 216, App	926	153.5	9.1	353	9	US-09-989-725-503	Sequence 503, App
854	158	352	14	US-10-219-074-216	Sequence 216, App	927	153.5	9.1	353	9	US-09-989-727-503	Sequence 503, App
855	158	352	14	US-10-219-077-216	Sequence 216, App	928	153.5	9.1	353	9	US-09-989-729-503	Sequence 503, App
856	158	352	14	US-10-219-465-216	Sequence 216, App	929	153.5	9.1	353	9	US-09-989-727-503	Sequence 503, App
857	158	352	14	US-10-219-467-216	Sequence 216, App	930	153.5	9.1	353	9	US-09-989-731-503	Sequence 503, App
858	158	352	14	US-10-219-469-216	Sequence 216, App	931	153.5	9.1	353	9	US-09-989-732-503	Sequence 503, App
859	158	352	14	US-10-219-471-216	Sequence 216, App	932	153.5	9.1	353	9	US-09-991-073-503	Sequence 503, App
860	158	352	14	US-10-219-473-216	Sequence 216, App	933	153.5	9.1	353	9	US-09-990-442-503	Sequence 503, App
861	158	352	14	US-10-219-476-216	Sequence 216, App	934	153.5	9.1	353	9	US-09-991-163-503	Sequence 503, App
862	158	352	14	US-10-219-482-216	Sequence 216, App	935	153.5	9.1	353	9	US-09-993-604-503	Sequence 503, App
863	158	352	14	US-10-227-874-216	Sequence 216, App	936	153.5	9.1	353	9	US-09-990-456-503	Sequence 503, App
864	158	352	14	US-10-227-876-216	Sequence 216, App	937	153.5	9.1	353	9	US-09-989-721-503	Sequence 503, App
865	158	352	14	US-10-227-878-216	Sequence 216, App	938	153.5	9.1	353	9	US-09-978-958-55	Sequence 59, App1
866	158	352	14	US-10-229-874-216	Sequence 216, App	939	153.5	9.1	353	9	US-09-992-598-503	Sequence 503, App
867	158	352	14	US-10-230-024-216	Sequence 216, App	940	153.5	9.1	353	9	US-09-978-97-59	Sequence 59, App1
868	158	352	14	US-10-230-113-216	Sequence 216, App	941	153.5	9.1	353	9	US-09-989-693A-503	Sequence 503, App
869	158	352	14	US-10-230-183-216	Sequence 216, App	942	153.5	9.1	353	9	US-09-978-192A-59	Sequence 59, App1
870	158	352	14	US-10-230-234-216	Sequence 216, App	943	153.5	9.1	353	9	US-09-993-687-503	Sequence 503, App
871	158	352	14	US-10-230-306-216	Sequence 216, App	944	153.5	9.1	353	10	US-09-989-734-503	Sequence 503, App
872	158	352	14	US-10-230-426-216	Sequence 216, App	945	153.5	9.1	353	10	US-09-978-189-59	Sequence 59, App1
873	158	352	14	US-10-230-427-216	Sequence 216, App	946	153.5	9.1	353	10	US-09-997-653-503	Sequence 503, App
874	158	352	14	US-10-230-433-216	Sequence 216, App	947	153.5	9.1	353	10	US-09-989-724-503	Sequence 503, App
875	158	352	14	US-10-230-435-216	Sequence 216, App	948	153.5	9.1	353	10	US-09-989-728-503	Sequence 503, App
876	158	352	14	US-10-230-438-216	Sequence 216, App	949	153.5	9.1	353	10	US-09-990-441-503	Sequence 503, App
877	158	352	14	US-10-232-222-216	Sequence 216, App	950	153.5	9.1	353	10	US-09-993-667-503	Sequence 503, App
878	158	352	14	US-10-232-084-280	Sequence 280, App	951	153.5	9.1	353	10	US-09-997-428-503	Sequence 503, App
879	158	352	14	US-10-223-088-280	Sequence 280, App	952	153.5	9.1	353	10	US-09-997-653-503	Sequence 503, App
880	158	352	14	US-10-223-090-280	Sequence 280, App	953	153.5	9.1	353	10	US-09-989-725-503	Sequence 503, App
881	158	352	14	US-10-219-070-216	Sequence 216, App	954	153.5	9.1	353	10	US-09-989-728-503	Sequence 503, App
882	158	352	14	US-10-219-472-216	Sequence 216, App	955	153.5	9.1	353	10	US-09-990-441-503	Sequence 503, App
883	158	352	14	US-10-219-527-216	Sequence 216, App	956	153.5	9.1	353	10	US-09-993-667-503	Sequence 503, App
884	158	352	14	US-10-227-877-216	Sequence 216, App	957	153.5	9.1	353	10	US-09-997-428-503	Sequence 503, App
885	158	352	14	US-10-223-087-280	Sequence 280, App	958	153.5	9.1	353	10	US-09-997-653-503	Sequence 503, App
886	158	352	14	US-10-223-083-280	Sequence 280, App	959	153.5	9.1	353	10	US-09-990-433-503	Sequence 503, App
887	158	352	14	US-10-216-166-216	Sequence 216, App	960	153.5	9.1	353	10	US-09-990-562-503	Sequence 503, App
888	158	352	14	US-10-218-612-216	Sequence 216, App	961	153.5	9.1	353	10	US-09-990-711-503	Sequence 503, App
889	158	352	14	US-10-223-069-280	Sequence 280, App	962	153.5	9.1	353	10	US-09-989-726-503	Sequence 503, App

963	153.5	9.1	373	10	US-09-998-156-503	Sequence 503, App	1036	153.5	9.1	373	14	US-10-176-921-388	Sequence 388, App
964	153.5	9.1	373	10	US-09-978-608A-59	Sequence 59, Appl	1037	153.5	9.1	373	14	US-10-227-884-130	Sequence 130, App
965	153.5	9.1	373	10	US-09-890-437-503	Sequence 503, App	1038	153.5	9.1	373	14	US-10-137-865-388	Sequence 388, App
966	153.5	9.1	373	10	US-09-878-585A-59	Sequence 59, Appl	1039	153.5	9.1	373	14	US-10-140-474-388	Sequence 388, App
967	153.5	9.1	373	10	US-09-991-157-503	Sequence 503, App	1040	153.5	9.1	373	14	US-10-142-431-388	Sequence 388, App
968	153.5	9.1	373	10	US-09-997-514-503	Sequence 503, App	1041	153.5	9.1	373	14	US-10-143-114-388	Sequence 388, App
969	153.5	9.1	373	10	US-09-997-573-503	Sequence 503, App	1042	153.5	9.1	373	14	US-10-230-163-130	Sequence 130, App
970	153.5	9.1	373	10	US-09-978-191A-59	Sequence 59, Appl	1043	153.5	9.1	373	14	US-10-140-002-388	Sequence 388, App
971	153.5	9.1	373	10	US-09-978-604A-59	Sequence 59, Appl	1044	153.5	9.1	373	14	US-10-230-338-130	Sequence 130, App
972	153.5	9.1	373	10	US-09-978-564A-59	Sequence 59, Appl	1045	153.5	9.1	373	14	US-10-142-419-388	Sequence 388, App
973	153.5	9.1	373	10	US-09-991-172-503	Sequence 503, App	1046	153.5	9.1	373	14	US-10-218-631-130	Sequence 130, App
974	153.5	9.1	373	10	US-09-990-726-503	Sequence 503, App	1047	153.5	9.1	373	14	US-10-011-081A-59	Sequence 59, Appl
975	153.5	9.1	373	10	US-09-997-559-503	Sequence 503, App	1048	153.5	9.1	373	14	US-10-123-262-388	Sequence 388, App
976	153.5	9.1	373	10	US-09-997-601-503	Sequence 503, App	1049	153.5	9.1	373	14	US-10-144-423-388	Sequence 388, App
977	153.5	9.1	373	10	US-09-999-833A-59	Sequence 59, Appl	1050	153.5	9.1	373	14	US-10-230-414-130	Sequence 130, App
978	153.5	9.1	373	10	US-09-981-915A-59	Sequence 59, Appl	1051	153.5	9.1	373	14	US-10-121-050-388	Sequence 388, App
979	153.5	9.1	373	10	US-09-990-443-503	Sequence 503, App	1052	153.5	9.1	373	14	US-10-141-755-388	Sequence 388, App
980	153.5	9.1	373	10	US-09-978-824-59	Sequence 59, Appl	1053	153.5	9.1	373	14	US-10-167-749-59	Sequence 59, Appl
981	153.5	9.1	373	10	US-09-991-854-503	Sequence 503, App	1054	153.5	9.1	373	14	US-10-143-032-388	Sequence 388, App
982	153.5	9.1	373	10	US-09-997-628-503	Sequence 503, App	1055	153.5	9.1	373	14	US-10-233-224-130	Sequence 130, App
983	153.5	9.1	373	10	US-09-997-683-503	Sequence 503, App	1056	153.5	9.1	373	14	US-10-013-921A-59	Sequence 59, Appl
984	153.5	9.1	373	10	US-09-989-728A-503	Sequence 503, App	1057	153.5	9.1	373	14	US-10-123-108-388	Sequence 388, App
985	153.5	9.1	373	10	US-09-997-349-503	Sequence 503, App	1058	153.5	9.1	373	14	US-10-123-226-388	Sequence 388, App
986	153.5	9.1	373	10	US-09-997-440-503	Sequence 503, App	1059	153.5	9.1	373	14	US-10-123-261-388	Sequence 388, App
987	153.5	9.1	373	10	US-09-918-585A-59	Sequence 59, Appl	1060	153.5	9.1	373	14	US-10-140-921-388	Sequence 388, App
988	153.5	9.1	373	10	US-09-990-440-503	Sequence 503, App	1061	153.5	9.1	373	14	US-10-140-928-388	Sequence 388, App
989	153.5	9.1	373	10	US-09-997-857-503	Sequence 503, App	1062	153.5	9.1	373	14	US-10-216-159A-130	Sequence 130, App
990	153.5	9.1	373	10	US-09-999-834A-59	Sequence 59, Appl	1063	153.5	9.1	373	14	US-10-011-929A-59	Sequence 59, Appl
991	153.5	9.1	373	10	US-09-993-469-503	Sequence 503, App	1064	153.5	9.1	373	14	US-10-016-117A-59	Sequence 59, Appl
992	153.5	9.1	373	10	US-09-997-542-503	Sequence 503, App	1065	153.5	9.1	373	14	US-10-121-045-388	Sequence 388, App
993	153.5	9.1	373	10	US-09-978-423A-59	Sequence 59, Appl	1066	153.5	9.1	373	14	US-10-123-292-388	Sequence 388, App
994	153.5	9.1	373	10	US-09-993-748-503	Sequence 503, App	1067	153.5	9.1	373	14	US-10-123-993-388	Sequence 388, App
995	153.5	9.1	373	10	US-09-990-439-503	Sequence 503, App	1068	153.5	9.1	373	14	US-10-124-819-388	Sequence 388, App
996	153.5	9.1	373	10	US-09-978-193A-59	Sequence 59, Appl	1069	153.5	9.1	373	14	US-10-124-822-388	Sequence 388, App
997	153.5	9.1	373	10	US-09-890-427-503	Sequence 503, App	1070	153.5	9.1	373	14	US-10-140-925-388	Sequence 388, App
998	153.5	9.1	373	10	US-09-989-328-503	Sequence 503, App	1071	153.5	9.1	373	14	US-10-160-488-388	Sequence 388, App
999	153.5	9.1	373	10	US-09-993-583-503	Sequence 503, App	1072	153.5	9.1	373	14	US-10-218-849-130	Sequence 130, App
1000	153.5	9.1	373	10	US-09-999-830A-59	Sequence 59, Appl	1073	153.5	9.1	373	14	US-10-227-873-130	Sequence 130, App
1001	153.5	9.1	373	10	US-09-941-992-503	Sequence 503, App	1074	153.5	9.1	373	14	US-10-227-883-130	Sequence 130, App
1002	153.5	9.1	373	10	US-09-978-757A-59	Sequence 59, Appl	1075	153.5	9.1	373	14	US-10-124-824-388	Sequence 388, App
1003	153.5	9.1	373	10	US-09-992-521-503	Sequence 503, App	1076	153.5	9.1	373	14	US-10-127-825A-388	Sequence 388, App
1004	153.5	9.1	373	10	US-09-997-333-503	Sequence 503, App	1077	153.5	9.1	373	14	US-10-127-829A-388	Sequence 388, App
1005	153.5	9.1	373	10	US-09-997-384-503	Sequence 503, App	1078	153.5	9.1	373	14	US-10-127-835A-388	Sequence 388, App
1006	153.5	9.1	373	10	US-09-978-187B-59	Sequence 59, Appl	1079	153.5	9.1	373	14	US-10-127-839A-388	Sequence 388, App
1007	153.5	9.1	373	10	US-09-978-643A-59	Sequence 59, Appl	1080	153.5	9.1	373	14	US-10-127-901A-388	Sequence 388, App
1008	153.5	9.1	373	10	US-09-998-041-503	Sequence 503, App	1081	153.5	9.1	373	14	US-10-128-633A-388	Sequence 388, App
1009	153.5	9.1	373	10	US-09-997-585-503	Sequence 503, App	1082	153.5	9.1	373	14	US-10-131-813A-388	Sequence 388, App
1010	153.5	9.1	373	10	US-09-997-614-503	Sequence 503, App	1083	153.5	9.1	373	14	US-10-131-818A-388	Sequence 388, App
1011	153.5	9.1	373	10	US-09-978-375A-59	Sequence 59, Appl	1084	153.5	9.1	373	14	US-10-131-823A-388	Sequence 388, App
1012	153.5	9.1	373	10	US-09-989-862-503	Sequence 503, App	1085	153.5	9.1	373	14	US-10-131-824A-388	Sequence 388, App
1013	153.5	9.1	373	10	US-09-997-529-503	Sequence 503, App	1086	153.5	9.1	373	14	US-10-131-830A-388	Sequence 388, App
1014	153.5	9.1	373	10	US-09-978-298A-59	Sequence 59, Appl	1087	153.5	9.1	373	14	US-10-131-837A-388	Sequence 388, App
1015	153.5	9.1	373	10	US-09-978-188A-59	Sequence 59, Appl	1088	153.5	9.1	373	14	US-10-137-872A-388	Sequence 388, App
1016	153.5	9.1	373	10	US-09-989-725-503	Sequence 503, App	1089	153.5	9.1	373	14	US-10-147-500-388	Sequence 388, App
1017	153.5	9.1	373	10	US-09-991-150-503	Sequence 503, App	1090	153.5	9.1	373	14	US-10-147-502-388	Sequence 388, App
1018	153.5	9.1	373	10	US-09-978-681A-59	Sequence 59, Appl	1091	153.5	9.1	373	14	US-10-147-515-388	Sequence 388, App
1019	153.5	9.1	373	10	US-09-978-194A-59	Sequence 59, Appl	1092	153.5	9.1	373	14	US-10-147-517-388	Sequence 388, App
1020	153.5	9.1	373	10	US-09-999-829A-59	Sequence 59, Appl	1093	153.5	9.1	373	14	US-10-147-526-388	Sequence 388, App
1021	153.5	9.1	373	10	US-09-978-299A-59	Sequence 59, Appl	1094	153.5	9.1	373	14	US-10-147-527-388	Sequence 388, App
1022	153.5	9.1	373	10	US-09-978-544A-59	Sequence 59, Appl	1095	153.5	9.1	373	14	US-10-121-041-388	Sequence 388, App
1023	153.5	9.1	373	10	US-09-978-665A-59	Sequence 59, Appl	1096	153.5	9.1	373	14	US-10-121-043-388	Sequence 388, App
1024	153.5	9.1	373	10	US-09-978-802A-59	Sequence 59, Appl	1097	153.5	9.1	373	14	US-10-121-047-388	Sequence 388, App
1025	153.5	9.1	373	10	US-09-997-641-503	Sequence 503, App	1098	153.5	9.1	373	14	US-10-123-215-388	Sequence 388, App
1026	153.5	9.1	373	10	US-09-989-733-503	Sequence 503, App	1099	153.5	9.1	373	14	US-10-123-992-388	Sequence 388, App
1027	153.5	9.1	373	10	US-09-992-643-503	Sequence 503, App	1100	153.5	9.1	373	14	US-10-123-998-388	Sequence 388, App
1028	153.5	9.1	373	11	US-09-999-831A-59	Sequence 59, Appl	1101	153.5	9.1	373	14	US-10-123-908-388	Sequence 388, App
1029	153.5	9.1	373	14	US-10-028-072-388	Sequence 388, App	1102	153.5	9.1	373	14	US-10-123-910-388	Sequence 388, App
1030	153.5	9.1	373	14	US-10-140-808-388	Sequence 388, App	1103	153.5	9.1	373	14	US-10-124-813-388	Sequence 388, App
1031	153.5	9.1	373	14	US-10-121-049-388	Sequence 388, App	1104	153.5	9.1	373	14	US-10-124-817-388	Sequence 388, App
1032	153.5	9.1	373	14	US-10-123-904-388	Sequence 388, App	1105	153.5	9.1	373	14	US-10-125-922-388	Sequence 388, App
1033	153.5	9.1	373	14	US-10-140-470-388	Sequence 388, App	1106	153.5	9.1	373	14	US-10-125-924-388	Sequence 388, App
1034	153.5	9.1	373	14	US-10-175-746-388	Sequence 388, App	1107	153.5	9.1	373	14	US-10-140-860-388	Sequence 388, App
1035	153.5	9.1	373	14	US-10-176-918-388	Sequence 388, App	1108	153.5	9.1	373	14	US-10-142-417-388	Sequence 388, App

1401	153.5	9.1	373	14	US-10-152-382-388	Sequence 388, App
1402	153.5	9.1	373	14	US-10-152-383-388	Sequence 388, App
1403	153.5	9.1	373	14	US-10-152-384-388	Sequence 388, App
1404	153.5	9.1	373	14	US-10-152-387-388	Sequence 388, App
1405	153.5	9.1	373	14	US-10-152-389-388	Sequence 388, App
1406	153.5	9.1	373	14	US-10-152-390-388	Sequence 388, App
1407	153.5	9.1	373	14	US-10-152-392-388	Sequence 388, App
1408	153.5	9.1	373	14	US-10-153-756-388	Sequence 388, App
1409	153.5	9.1	373	14	US-10-157-784-388	Sequence 388, App
1410	153.5	9.1	373	14	US-10-157-797-388	Sequence 388, App
1411	153.5	9.1	373	14	US-10-158-491-388	Sequence 388, App
1412	153.5	9.1	373	14	US-10-143-028A-59	Sequence 59, Appl
1413	153.5	9.1	373	14	US-10-143-029A-59	Sequence 59, Appl
1414	153.5	9.1	373	14	US-10-142-762-388	Sequence 388, App
1415	153.5	9.1	373	14	US-10-142-764-388	Sequence 388, App
1416	153.5	9.1	373	14	US-10-142-766-388	Sequence 388, App
1417	153.5	9.1	373	14	US-10-145-089A-59	Sequence 59, Appl
1418	153.5	9.1	373	14	US-10-145-625-388	Sequence 388, App
1419	153.5	9.1	373	14	US-10-145-627-388	Sequence 388, App
1420	153.5	9.1	373	14	US-10-145-960-388	Sequence 388, App
1421	153.5	9.1	373	14	US-10-145-962-388	Sequence 388, App
1422	153.5	9.1	373	14	US-10-146-789-388	Sequence 388, App
1423	153.5	9.1	373	14	US-10-147-483-388	Sequence 388, App
1424	153.5	9.1	373	14	US-10-147-496-388	Sequence 388, App
1425	153.5	9.1	373	14	US-10-147-505-388	Sequence 388, App
1426	153.5	9.1	373	14	US-10-147-516-388	Sequence 388, App
1427	153.5	9.1	373	14	US-10-152-398-388	Sequence 388, App
1428	153.5	9.1	373	14	US-10-139-980-388	Sequence 388, App
1429	153.5	9.1	373	14	US-10-165-067A-59	Sequence 59, Appl
1430	153.5	9.1	373	14	US-10-145-017A-59	Sequence 59, Appl
1431	153.5	9.1	373	14	US-10-152-373-388	Sequence 388, App
1432	153.5	9.1	373	14	US-10-164-728A-59	Sequence 59, Appl
1433	153.5	9.1	373	14	US-10-223-081-64	Sequence 64, Appl
1434	153.5	9.1	373	14	US-10-218-765-130	Sequence 130, App
1435	153.5	9.1	373	14	US-10-219-063-130	Sequence 130, App
1436	153.5	9.1	373	14	US-10-219-066-130	Sequence 130, App
1437	153.5	9.1	373	14	US-10-219-067-130	Sequence 130, App
1438	153.5	9.1	373	14	US-10-219-068-130	Sequence 130, App
1439	153.5	9.1	373	14	US-10-219-069-130	Sequence 130, App
1440	153.5	9.1	373	14	US-10-219-073-130	Sequence 130, App
1441	153.5	9.1	373	14	US-10-219-483-130	Sequence 130, App
1442	153.5	9.1	373	14	US-10-219-485-130	Sequence 130, App
1443	153.5	9.1	373	14	US-10-219-525-130	Sequence 130, App
1444	153.5	9.1	373	14	US-10-219-526-130	Sequence 130, App
1445	153.5	9.1	373	14	US-10-219-530-130	Sequence 130, App
1446	153.5	9.1	373	14	US-10-219-531-130	Sequence 130, App
1447	153.5	9.1	373	14	US-10-219-532-130	Sequence 130, App
1448	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1449	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1450	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1451	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1452	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1453	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1454	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1455	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1456	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1457	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1458	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1459	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1460	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1461	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1462	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1463	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1464	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1465	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1466	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1467	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1468	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1469	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1470	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1471	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1472	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1473	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App

Search completed: January 4, 2005, 06:24:33
Job time : 561 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6

OM protein - protein search, using SW model
 Run on: January 4, 2005, 06:10:27 Search time 89 Seconds
 (without alignments)
 1293.844 Million cell updates/sec

Title: US-10-767-374-2

Perfect score: 1688

Sequence: 1 MGILLGLLGLHITVDYGR.....AYIMLCRKTSQGEHYEAR 321
 Scoring table: BLOSUM62

Searched: 2002273 seqs, 358729299 residues
 Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Database: A_Geneseq_23Sep04.*
 Listing first 1500 summaries

1: geneseqp1980s.*
 2: geneseqp1980s.*
 3: geneseqp2000s.*
 4: geneseqp2001s.*
 5: geneseqp2002s.*
 6: geneseqp2003as.*
 7: geneseqp2003bs.*
 8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
-----	-------	-------	--------	----	----	-------------

RESULT 1: AAY23322 standard; protein; 321 AA.
 DE Amino acid sequence of the PRO362 polypeptide.

PN WO9927098-A2.
 PD 03-JUN-1999.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 2; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 2: AAY41691 standard; protein; 321 AA.
 DE Human PRO 362 protein sequence.

PN WO9946281-AZ.
 PD 16-SEP-1999.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 2; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 3: AAB33429 standard; protein; 321 AA.
 DE Human PRO362 protein UNQ317 SEQ ID NO:80.

PN WO200053758-A2.
 PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 3; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 4: AAB44247 standard; protein; 321 AA.
 DE Human PRO362 (UNQ317) protein sequence SEQ ID NO:52.

PN WO200053756-A2.
 PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 3; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 5: AAY95346 standard; protein; 321 AA.
 DE Human PRO362 antitumour protein.

PN WO200037463-A2.
 PD 29-JUN-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 3; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 6: AAB24047 standard; protein; 321 AA.

DE Human PRO362 protein sequence SEQ ID NO:14.

PN WO200053754-A1.
 PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 3; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 7: ABO25193 standard; protein; 321 AA.
 DE Novel human secreted and transmembrane protein PRO362.

PN US2003050239-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 8: ABO72199 standard; protein; 321 AA.
 DE Novel human secreted and transmembrane protein PRO362.

PN US2002192706-A1.
 PD 19-DEC-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 9: ABO84879 standard; protein; 321 AA.
 DE Human secreted and transmembrane polypeptide PRO362.

PN US2002177553-A1.
 PD 28-NOV-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 10: ABO61077 standard; protein; 321 AA.
 DE Human PRO362 polypeptide.

PN US2002169284-A1.
 PD 14-NOV-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 11: ABO80346 standard; protein; 321 AA.
 DE Human secreted/transmembrane protein PRO362.

PN US2003004102-A1.
 PD 02-JAN-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 12: ABO07737 standard; protein; 321 AA.
 DE Human A-33 related antigen PRO362.

PN US2002182206-A1.
 PD 05-DEC-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 13: ADB24591 standard; protein; 321 AA.
 DE Novel human secreted and transmembrane protein PRO362.

PN US2003050241-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 14: ABO19648 standard; protein; 321 AA.
 DE Novel human secreted and transmembrane protein PRO362.

PN US2003050240-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 15: ADA12252 standard; protein; 321 AA.
 DE Human secreted/transmembrane polypeptide PRO362.

PN US2003055216-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 16
ID ABO19539 standard; protein; 321 AA.
DE Novel human secreted and transmembrane polypeptide #7.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 17
ID ADB71558 standard; protein; 321 AA.
DE Human PRO polypeptide #7.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 18
ID ADB76274 standard; protein; 321 AA.
DE Human PRO polypeptide #7.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 19
ID ADC43700 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 20
ID ADC61460 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 21
ID ADC63424 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 22
ID ADC65524 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 23
ID ADC68648 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 24
ID ADC62708 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003068648-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 25
ID ADC67773 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 26
ID ADC41093 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 27
ID ADC67148 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 28
ID ADC62084 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 29
ID ADC41717 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 30
ID ADC78883 standard; protein; 321 AA.
DE Human PRO protein #56.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 31
ID ADE49086 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 32
ID ADE35140 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 33
ID ADE16254 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match	100.0%;	Score 1688;	DB 7;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 34				
ID	ADD72869 standard; protein, 321 AA.			
DE	Human secreted/cranmembrane protein, PRO362.			
PN	US2003203436-A1.			
PD	30-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1688;	DB 7;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 35				
ID	ADD72227 standard; protein, 321 AA.			
DE	Human secreted/cranmembrane protein, PRO362.			
PN	US2003194781-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1688;	DB 7;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 36				
ID	AD616878 standard; protein, 321 AA.			
DE	Human secreted/cranmembrane protein, PRO362.			
PN	US2003203433-A1.			
PD	30-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1688;	DB 7;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 37				
ID	ADP46892 standard; protein, 321 AA.			
DE	Human secreted/cranmembrane protein, PRO362.			
PN	US2003195333-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1688;	DB 7;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 38				
ID	ADG52649 standard; protein, 321 AA.			
DE	Human secreted/cranmembrane protein, PRO362.			
PN	US2003216561-A1.			
PD	20-NOV-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1688;	DB 7;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 39				
ID	ADG59969 standard; protein, 321 AA.			
DE	Human secreted/cranmembrane protein, PRO362.			
PN	US2003206915-A1.			
PD	06-NOV-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1688;	DB 7;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 40				
ID	ADH62529 standard; protein, 321 AA.			
DE	Human secreted/cranmembrane protein, PRO362.			
PN	US2003171568-A1.			
PD	11-SEP-2003.			
PA	(ASHK/) ASHKENAZI A.			
PA	(FONG/) FONG S.			
PA	(GODD/) GODDARD A.			
PA	(GURN/) GURNAY A L.			
PA	(NAPI/) NAPIER M A.			
PA	(TUMA/) TUMAS D.			
PA	(WOOD/) WOOD W I.			
Query Match	100.0%;	Score 1688;	DB 7;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 41				
ID	ADI60729 standard; protein, 321 AA.			
DE	Human secreted/cranmembrane protein, PRO362.			
PN	US2003077700-A1.			
PD	24-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1688;	DB 7;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 42				
ID	ADJ4386 standard; protein, 321 AA.			
DE	Human secreted/cranmembrane protein, PRO362.			
PN	US2003104536-A1.			
PD	05-JUN-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1688;	DB 8;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 43				
ID	AD69487 standard; protein, 321 AA.			
DE	Human secreted/cranmembrane protein, PRO362.			
PN	US2003130181-A1.			
PD	10-UTL-2003.			
PA	(ASHK/) ASHKENAZI A J.			
PA	(BAKE/) BAKER K P.			
PA	(BOTS/) BOTSTEIN D.			
PA	(DESN/) DESNOYERS L.			
PA	(EATO/) EATON D L.			
PA	(FERR/) FERRARA N.			
PA	(FILV/) FILVAROFF E.			
PA	(FONG/) FONG S.			
PA	(GAOW/) GAO W.			
PA	(GERB/) GERBER H.			
PA	(GERB/) GERRTSEN M E.			
PA	(GODD/) GODDARD A.			
PA	(GODO/) GODOWSKI P J.			
PA	(GIRM/) GIRMALDI J C.			
PA	(GURN/) GURNAY A L.			
PA	(HILL/) HILLAN K J.			
PA	(KLAJ/) KLAJAVIN I J.			
PA	(KUOS/) KUO S S.			
PA	(NAPI/) NAPIER M A.			
PA	(PANJ/) PAN J.			
PA	(PAON/) PAONI N F.			

ID	ADP48386	standard; protein; 321 AA.		
DE	Human secreted/transmembrane protein, PRO362.			
PN	US2003104536-A1.			
PD	05-JUN-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1688;	DB 8;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 43				
ID	ADBE9487	standard; protein; 321 AA.		
DE	Human secreted/transmembrane protein, PRO362.			
PN	US2003130181-A1.			
PD	10-JUL-2003.			
PA	(ASHK/) ASHKENAZI A J.			
PA	(BAKE/) BAKER K P.			
PA	(BOTS/) BOTSTEIN D.			
PA	(DESN/) DESNOYERS L.			
PA	(EATO/) EATON D L.			
PA	(FERR/) FERRARA N.			
PA	(FILV/) FILVAROFF E.			
PA	(FONG/) FONG S.			
PA	(GAOW/) GAO W.			
PA	(GERB/) GERBER H.			
PA	(GERR/) GERRTSEN M E.			
PA	(GODD/) GODDARD A.			
PA	(GODO/) GODOWSKI P J.			
PA	(GIRM/) GIRMALDI J C.			
PA	(GURN/) GURNEY A L.			
PA	(HILL/) HILLAN K J.			
PA	(KJJA/) KJAVVIN I J.			
PA	(KUOS/) KUO S S.			
PA	(NAPI/) NAPIER M A.			
PA	(NANI/) PANI J.			
PA	(PAON/) PAONI N F.			
PA	(ROYM/) ROY M A.			
PA	(SHEL/) SHELTON D L.			
PA	(STEM/) STEWART T A.			
PA	(TUMA/) TUMAS D.			
PA	(WILL/) WILLIAMS P M.			
PA	(WOOD/) WOOD W I.			
Query Match	100.0%;	Score 1688;	DB 8;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 44				
ID	ADFE1127	standard; protein; 321 AA.		
DE	Human secreted/transmembrane protein, PRO362.			
PN	US2003195345-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1688;	DB 8;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 45				
ID	ADPF9819	standard; protein; 321 AA.		
DE	Human secreted/transmembrane protein, PRO362.			
PN	US2003198994-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1688;	DB 8;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 46				
ID	ADFA5615	standard; protein; 321 AA.		
DE	Human secreted/transmembrane protein, PRO362.			
PN	US2003195148-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1688;	DB 8;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
RESULT 47				
ID	ADFP4011	standard; protein; 321 AA.		
DE	Human secreted/transmembrane protein, PRO362.			
PN	US2003204055-A1.			
PD	30-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1688;	DB 8;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		
Query Match	100.0%;	Score 1688;	DB 8;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 9e-136;		

```
RESULT 48
ID ADF40443 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 49
ID ADF23387 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 50
ID ADF33370 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 51
ID ADF26837 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 52
ID ADF27473 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 53
ID ADF41067 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 54
ID ADF3746 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 55
ID ADF25112 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 56
ID ADF26213 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 57
ID ADF34002 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 58
ID ADF46239 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 59
ID ADG50225 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 60
ID ADG49601 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 61
ID ADG51473 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 62
ID ADG48977 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 63
ID ADG48353 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 64
ID ADG50849 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 65
ID ADG58793 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 66
ID ADG62249 standard; protein; 321 AA.
```

DE Human secreted/cranmembrane protein, PRO362.
PN US200406219-A1.
PD 08-JAN-2004.
PA (HUMA-) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 8; Length 321;
RESULT 67
ID ADR25274 standard; protein, 321 AA.
DE Human neurotrophin homologue related protein sequence SEQ ID NO:52.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 8; Length 321;
RESULT 68
ID ADM17051 standard; protein, 321 AA.
DE Human secreted/cranmembrane protein, PRO362.
PN US200404832-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 8; Length 321;
RESULT 69
ID ADL06885 standard; protein, 321 AA.
DE Human secreted/cranmembrane protein, PRO362.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 8; Length 321;
RESULT 70
ID ADN35285 standard; protein, 321 AA.
DE Human STRIGA protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 8; Length 321;
RESULT 71
ID AAB19396 standard; protein, 399 AA.
DE Amino acid sequence of a human secreted protein.
PN WO2000061755-A2.
PD 19-OCT-2000.
PA (CHIR) CHIRON CORP.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 3; Length 399;
RESULT 72
ID AAB04230 standard; protein, 399 AA.
DE Human gene 11 encoded secreted protein HMSOM51, SEQ ID NO:85.
PN WO200136432-A2.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 4; Length 399;
RESULT 73
ID AAE04208 standard; protein, 399 AA.
DE Human gene 11 encoded secreted protein HMSOM51, SEQ ID NO:63.
PN WO200136432-A2.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 4; Length 399;
RESULT 74
ID ABG6448 standard; protein, 399 AA.
DE Human albumin fusion protein #1163.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 5; Length 399;
RESULT 75
ID ABG6448 standard; protein, 399 AA.
DE Human albumin fusion protein #1162.

PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 5; Length 399;
RESULT 76
ID ABU03567 standard; protein, 399 AA.
DE Angiogenesis-associated human protein sequence #112.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (BOSB-) BOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 6; Length 399;
RESULT 77
ID ADA57183 standard; protein, 399 AA.
DE Human secreted protein #466.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 6; Length 399;
RESULT 78
ID ADA41052 standard; protein, 399 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 6; Length 399;
RESULT 79
ID ABR47904 standard; protein, 399 AA.
DE Human secreted protein, SEQ ID 795.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 6; Length 399;
RESULT 80
ID ABR00157 standard; protein, 399 AA.
DE Human gene 147 encoded secreted protein HSDK49, SEQ ID NO:446.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 6; Length 399;
RESULT 81
ID ADB91646 standard; protein, 399 AA.
DE Human secreted protein #SEQ ID 592.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 7; Length 399;
RESULT 82
ID ADC74298 standard; protein, 399 AA.
DE Human secreted protein - SEQ ID 931.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 7; Length 399;
RESULT 83
ID ADL77755 standard; protein, 399 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1237.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 8; Length 399;
RESULT 84
ID ADL77754 standard; protein, 399 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1236.

PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 100.0%; Score 1688; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 85
ID ADL67172 standard; protein; 399 AA.
DE Human B7-H6 protein SEQ ID NO:42.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 100.0%; Score 1688; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 86
ID ADN3531 standard; protein; 399 AA.
DE Human STIGMA protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 87
ID AAM33874 standard; protein; 399 AA.
DE Human polypeptide; SEQ ID NO: 3986.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.5%; Score 1680; DB 4; Length 399;
Best Local Similarity 99.4%; Pred. No. 5.8e-135;
RESULT 88
ID ADL31953 standard; protein; 399 AA.
DE Human protein encoded by a full length cDNA clone seqid 3986.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 99.5%; Score 1680; DB 8; Length 399;
Best Local Similarity 99.4%; Pred. No. 5.8e-135;
RESULT 89
ID AAB04290 standard; protein; 386 AA.
DE Human gene 11 encoded secreted protein fragment, SEQ ID NO:154.
PN WO200136432-A2.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 96.3%; Score 1625; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.8e-130;
RESULT 90
ID ADL67174 standard; protein; 281 AA.
DE Human B7-H6 (ECD) protein SEQ ID NO:44.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 87.7%; Score 1480; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 4.6e-118;
RESULT 91
ID ADA57531 standard; protein; 305 AA.
DE Human secreted protein #66.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.4%; Score 1137; DB 6; Length 305;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 92
ID ADA41415 standard; protein; 305 AA.
DE Human secreted protein.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.4%; Score 1137; DB 6; Length 305;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 93
ID ABR46114 standard; protein; 305 AA.
DE Human secreted protein, SEQ ID 1005.

PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.4%; Score 1137; DB 6; Length 305;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 94
ID ABR00282 standard; protein; 305 AA.
DE Human gene 147 encoded secreted protein HSDEK49, SEQ ID NO:571.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.4%; Score 1137; DB 6; Length 305;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 95
ID ADB91804 standard; protein; 305 AA.
DE Human secreted protein HSEQ ID 750.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.4%; Score 1137; DB 7; Length 305;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 96
ID ADC74547 standard; protein; 305 AA.
DE Human secreted protein - SEQ ID 1180.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.4%; Score 1137; DB 7; Length 305;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 97
ID ADN35312 standard; protein; 305 AA.
DE Human short STIGMA protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 67.4%; Score 1137; DB 8; Length 305;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 98
ID AAY30814 standard; protein; 306 AA.
DE Human secreted protein encoded from gene 4.
PN WO9940100-A1.
PD 12-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.4%; Score 1137; DB 2; Length 306;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 99
ID AAM93588 standard; protein; 184 AA.
DE Human polypeptide; SEQ ID NO: 3387.
PN EP1396543-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 58.2%; Score 983; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 8.4e-76;
RESULT 100
ID ADL1354 standard; protein; 184 AA.
DE Human protein encoded by a full length cDNA clone seqid 3387.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 58.2%; Score 983; DB 8; Length 184;
Best Local Similarity 100.0%; Pred. No. 8.4e-76;
RESULT 101
ID AAY62322 standard; protein; 175 AA.
DE Human protein transport molecule (PTM) SEQ ID NO:6.
PN WO200012703-A2.
PD 09-MAR-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 51.5%; Score 870; DB 3; Length 175;
Best Local Similarity 64.7%; Pred. No. 3.6e-66;
RESULT 102
ID ADK70486 standard; protein; 175 AA.
DE Respiratory disease differentially expressed protein #52.
PN WO2003101283-A2.

PD 11-DEC-2003.
PA (INCY-) INCTE CORP.
Query Match 51.5%; Score 870; DB 8; Length 175;
Best Local Similarity 64.7%; Pred. No. 3.6e-66;
RESULT 103
ID ADL67144 standard; protein; 280 AA.
DE Mouse B7-H6 protein SEQ ID NO:14.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 43.1%; Score 728; DB 8; Length 280;
Best Local Similarity 47.0%; Pred. No. 9.6e-54;
RESULT 104
ID ADN35313 standard; protein; 280 AA.
DE Murine STIGMA protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 43.1%; Score 728; DB 8; Length 280;
Best Local Similarity 47.0%; Pred. No. 9.6e-54;
RESULT 105
ID ADL67146 standard; protein; 188 AA.
DE Mouse B7-H6(ECD) protein SEQ ID NO:16.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 36.3%; Score 613; DB 8; Length 188;
Best Local Similarity 45.7%; Pred. No. 3.8e-44;
RESULT 106
ID AAE10596 standard; protein; 93 AA.
DE Human macrophage-expressed protein #21.
PN WO200164839-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 29.1%; Score 492; DB 4; Length 93;
Best Local Similarity 98.9%; Pred. No. 3.3e-34;
RESULT 107
ID ADH80723 standard; protein; 300 AA.
DE Human polypeptide #40.
PN US200323054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRMA/) DRMANAC R T.
Query Match 10.7%; Score 180; DB 8; Length 300;
Best Local Similarity 27.9%; Pred. No. 7.8e-07;
RESULT 108
ID AAY23321 standard; protein; 299 AA.
DE Amino acid sequence of the PRO301 polypeptide.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH-) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 109
ID AAW74464 standard; protein; 299 AA.
DE F11 antigen protein sequence.
PN WO9902561-A1.
PD 21-JAN-1999.
PA (SMIX-) SMITHKLINE BEECHAM CORP.
Query Match 10.6%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 110
ID AAY08071 standard; protein; 299 AA.
DE Human PRO307 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 111
ID AAY13364 standard; protein; 299 AA.
DE Amino acid sequence of protein PRO301.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 112
ID AAY76011 standard; protein; 299 AA.
DE Human A33 receptor homologue, SEQ ID NO:189.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.6%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 113
ID AAY76076 standard; protein; 299 AA.
DE Human A33 receptor homologue, SEQ ID NO:331.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.6%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 114
ID AAY70670 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO20015797-A2.
PD 23-MAR-2000.
PA (GETH-) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 115
ID AAB24405 standard; protein; 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:90.
PN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH-) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 116
ID AAY95344 standard; protein; 299 AA.
DE Human PRO301 antitumour protein.
PN WO200037638-A2.
PD 29-JUN-2000.
PA (GETH-) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 117
ID AAB80232 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH-) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 118
ID AAW93577 standard; protein; 299 AA.
DE Human polypeptide, SEQ ID NO: 3365.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 119
ID AAB56015 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 331.
PN WO200069884-A2.

PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 120
ID AAB55950 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 189.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 121
ID AAB31202 standard; protein; 299 AA.
DE Amino acid sequence of human polypeptide PRO301.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 122
ID AAU00823 standard; protein; 299 AA.
DE Human immune response protein PRO301 (UNQ264).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 123
ID AAU12354 standard; protein; 299 AA.
DE Human PRO301 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 124
ID AAB51086 standard; protein; 299 AA.
DE Human angiotensin-associated protein PRO301, SEQ ID NO:119.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 125
ID AAU14405 standard; protein; 299 AA.
DE Human novel protein #276.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 126
ID AAU14404 standard; protein; 299 AA.
DE Human novel protein #275.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 127
ID AAU14168 standard; protein; 299 AA.
DE Human novel protein #39.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 128
ID AAB03896 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein fragment, SEQ ID NO:148.
PN WO200136440-A1.
PD 25-MAY-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 129
ID AAE03840 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein HMA29, SEQ ID NO: 86.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 130
ID AAE03870 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein HMA29, SEQ ID NO:116.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 131
ID ABB90290 standard; protein; 299 AA.
DE Human polypeptide SEQ ID NO 2666.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 132
ID ABB84843 standard; protein; 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:54.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 133
ID ABB64551 standard; protein; 299 AA.
DE Human albumin fusion protein #1226.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 134
ID ABB64552 standard; protein; 299 AA.
DE Human albumin fusion protein #1227.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 135
ID ABB72215 standard; protein; 299 AA.
DE Human protein isolated from skin cells SEQ ID NO: 331.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.6%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 136
ID ABB72150 standard; protein; 299 AA.
DE Human protein isolated from skin cells SEQ ID NO: 189.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.6%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 137
ID ABB96449 standard; protein; 299 AA.
DE Human angiotensin related protein PRO301 SEQ ID NO: 54.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.

PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERR/) GERBER H.
PA (GERR/) GERITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MASTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.6%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 138
ID ABU71610 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 139
ID ABO17798 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 140
ID ABU71465 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 141
ID ABO25173 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 142
ID ABU81052 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 143
ID ABU71911 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 144
ID ABO01794 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;

RESULT 145
ID ABU66752 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 146
ID ABU54367 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 147
ID ABU67291 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 148
ID ABO47382 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 149
ID ABU59633 standard; protein; 299 AA.
DE Novel secreted and transmembrane protein PRO301.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 150
ID ABO25023 standard; protein; 299 AA.
DE Human secreted/transmembrane protein (PRO) #183.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 151
ID ABU64519 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #23.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 152
ID ABU72059 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 153
ID ABU67365 standard; protein; 299 AA.
DE Human secreted protein PRO301.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 154

ID ABU67160 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 155
ID ABO14885 standard; protein; 299 AA.
DE Human secreted / transmembrane polypeptide PRO301.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 156
ID ABU07736 standard; protein; 299 AA.
DE Human A-33 related antigen PRO301.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 157
ID AAO16451 standard; protein; 299 AA.
DE Human junctional adhesion molecule 1 (hujAM1).
PN WO2003008541-A2.
PD 30-JAN-2003.
PA (ELLY) LILLY & CO ELI.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 158
ID ABU67028 standard; protein; 299 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 366.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 159
ID ABU6642 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 160
ID ABU79802 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 161
ID ABO14824 standard; protein; 299 AA.
DE Human secreted / transmembrane polypeptide PRO301.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 162
ID ADA45885 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 163
ID ADA76316 standard; protein; 299 AA.

DE Human PRO polypeptide #183.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 164
ID ADB29324 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 165
ID ADA18966 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 166
ID ADA61589 standard; protein; 299 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 167
ID ADB19374 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 168
ID ADB27915 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 169
ID ADA86394 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 170
ID ADB15958 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 171
ID ADA47744 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 172
ID ADA18180 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.

PN US200303971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 173
ID ABO32776 standard; protein: 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 174
ID ADA67539 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 175
ID ADB30546 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 176
ID ADA8542 standard; protein: 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 177
ID ADA97054 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 178
ID ADA79358 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 179
ID ADA87497 standard; protein: 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 180
ID ADB16699 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 181
ID ABO43636 standard; protein: 299 AA.
DE Human PRO polypeptide #21.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 182
ID ADA16155 standard; protein: 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003048621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 183
ID ADA91791 standard; protein: 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 184
ID ADB14654 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 185
ID ADA47263 standard; protein: 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 186
ID ADB18615 standard; protein: 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 187
ID ADA94030 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 188
ID ADB19926 standard; protein: 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 189
ID ADB13238 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 190
ID ABO43331 standard; protein: 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003044945-A1.
PD 06-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 191
ID ADA74492 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 192
ID ADA42300 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 193
ID ADB24725 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 194
ID ADA82249 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 195
ID ADA75212 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 196
ID ADA85290 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 197
ID ADA84738 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 198
ID ABO17514 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 199
ID ADB23994 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 200
ID ADA80522 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 201
ID ADA75764 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 202
ID ADA46989 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 203
ID ADB25285 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 204
ID ADA93461 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 205
ID ADB26811 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030932147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 206
ID ADB31098 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 207
ID ADA61026 standard; protein; 299 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 208
ID ADB24173 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 209
ID ADB24173 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;

Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 209
ID ADA96502 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 210
ID ADA81074 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 211
ID ADA95950 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 212
ID ADB26259 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 213
ID ADB2144 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 214
ID ADA77523 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 215
ID ADB18263 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 216
ID ADA86946 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 217
ID ADA16579 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 218
ID ADA13008 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 219
ID ADA41876 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 220
ID ADA8049 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 221
ID ADA46437 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 222
ID ADA17223 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 223
ID ADA42726 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 224
ID ADB28467 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 225
ID ADB29019 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 226
ID ADA76971 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 227

ID ADA88601 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 228
ID ADA97606 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 229
ID ADB27363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 230
ID ADB22296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 231
ID ABO19860 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO302.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 232
ID ABO17575 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 233
ID ADA66987 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 234
ID ADB22848 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 235
ID ADB23621 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 236
ID ADA93343 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082712-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 237
ID ADB15406 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 238
ID ADB36658 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 239
ID ADB38106 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 240
ID ADB66578 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 241
ID ADB89658 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082658-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 242
ID ADB90390 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 243
ID ADB77645 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 244
ID ADB39491 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 245
ID ADB74781 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003082542-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 246				
ID ADB347114 standard; protein; 299 AA.				
DE Novel human secreted and transmembrane protein PRO301.				
PN US2003082687-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 247				
ID ADB86721 standard; protein; 299 AA.				
DE Human PRO polypeptide #183.				
PN US2003082697-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 248				
ID ADB77326 standard; protein; 299 AA.				
DE Novel human secreted and transmembrane protein PRO301.				
PN US2003082696-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 249				
ID ADB344483 standard; protein; 299 AA.				
DE Human PRO polypeptide SEQ ID NO 366.				
PN US2003077719-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 250				
ID ADB35587 standard; protein; 299 AA.				
DE Human PRO polypeptide SEQ ID NO 366.				
PN US2003077719-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 251				
ID ADB33931 standard; protein; 299 AA.				
DE Human PRO polypeptide SEQ ID NO 366.				
PN US2003077716-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 252				
ID ADB35035 standard; protein; 299 AA.				
DE Human PRO polypeptide SEQ ID NO 366.				
PN US2003077718-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 253				
ID ADB36139 standard; protein; 299 AA.				
DE Human PRO polypeptide SEQ ID NO 366.				
PN US2003077720-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 254				
ID ADB46534 standard; protein; 299 AA.				
DE Novel human secreted and transmembrane protein PRO301.				
PN US2003082692-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 255				
ID ADC28427 standard; protein; 299 AA.				
DE Human secreted/transmembrane protein, #25.				
PN US2003059772-A1.				
PD 27-MAR-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 256				
ID ADC39627 standard; protein; 299 AA.				
DE Human secreted/transmembrane protein, #25.				
PN US2003059828-A1.				
PD 27-MAR-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 257				
ID ADC40141 standard; protein; 299 AA.				
DE Human secreted/transmembrane protein, #25.				
PN US2003059829-A1.				
PD 27-MAR-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 258				
ID ADC18969 standard; protein; 299 AA.				
DE Human secreted/transmembrane protein, #25.				
PN US2003036061-A1.				
PD 20-FEB-2003.				

Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 264		
ID	ADCC3841 standard; protein; 299 AA.	
DE	Human secreted/transmembrane protein, #25.	
PN	US2003073077-A1.	
PD	17-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 265		
ID	ADCI2911 standard; protein; 299 AA.	
DE	Human secreted/transmembrane protein, #25.	
PN	US2003073079-A1.	
PD	17-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 266		
ID	ADCC5407 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein PRO301.	
PN	US2003092106-A1.	
PD	15-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 267		
ID	ADCT1954 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein PRO301.	
PN	US2003092107-A1.	
PD	15-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 268		
ID	ADCS9933 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein PRO301.	
PN	US2003092105-A1.	
PD	15-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 269		
ID	ADCS2940 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein Seq ID366.	
PN	US2003087365-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 270		
ID	ADCS7294 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein Seq ID366.	
PN	US2003087366-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 271		
ID	ADCC6485 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein PRO301.	
PN	US2003087367-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 272		
ID	ADCS0960 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein PRO301.	
PN	US2003087361-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 273		
ID	ADCS0960 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein PRO301.	
PN	US2003087361-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;

RESULT 273	ID ADC65487 standard; protein; 299 AA.
PD Human PRO polypeptide #183.	
PN US2003087362-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 274	ID ADC54585 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seg ID366.	
PN US2003087363-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 275	ID ADC53546 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seg ID366.	
PN US2003087364-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 276	ID ADC59069 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seg ID366.	
PN US2003087359-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 277	ID ADC55947 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seg ID366.	
PN US2003087360-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 278	ID ADC58517 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seg ID366.	
PN US2003087346-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 279	ID ADCL2363 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.	
PN US2003082541-A1.	
PD 01-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 280	ID ADL30191 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.	
PN US2003092104-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 281	ID ADC90183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.	
PN US2003087348-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 282	ID ADC90183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.	
PN US2003087348-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 282	ID ADC90183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.	
PN US2003087348-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;

ID ADC69602 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PD US2003194770-A1.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 283
ID ADC48491 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PD US2003194773-A1.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 284
ID ADD10020 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PD US2003194776-A1.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 285
ID ADD04595 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PD US2003087354-A1.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 286
ID ADC80551 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 287
ID ADD11058 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PD US2003194774-A1.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 288
ID ADD10343 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 289
ID ADC47939 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PD US2003194771-A1.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 290
ID ADD04918 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PD US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 291
ID ADC79999 standard; protein; 299 AA.

DE Novel human secreted and transmembrane protein PRO301.
PD US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 292
ID ADD11303 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PD US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 293
ID ADD09468 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PD US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 294
ID ADD03924 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PD US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 295
ID ADD03500 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PD US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 296
ID ADD41181 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PD US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 297
ID ADD52320 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PD US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 298
ID ADD53060 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PD US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 299
ID ADD53612 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PD US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 300
ID ADD37096 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.

PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 301
ID ADD51768 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 302
ID ADD02567 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 303
ID ADD02001 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 304
ID ADD54183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 305
ID ADD92500 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003198030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 306
ID ADD91396 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 307
ID ADE04010 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 308
ID ADE33307 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 309
ID ADE22239 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 310
ID ADE17816 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 311
ID ADE41999 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 312
ID ADE17816 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 313
ID ADD91948 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 314
ID ADE33411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 315
ID ADE33963 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 316
ID ADD80015 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 317
ID ADD93052 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 318
ID ADE19472 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199025-A1.
PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 319
ID ADE34752 standard; protein; 299 AA.
DE Human secreted/cranemembrane protein, #25.
PN US2003077583-A1.
PD 24-APR-2003
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 320
ID ADE18920 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 321
ID ADE43116 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 322
ID ADE95905 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 323
ID ADE22791 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 324
ID ADE78909 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 325
ID ADE32859 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 326
ID ADE42551 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 327
ID ADE80567 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 328
ID ADE89595 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 329
ID ADE40879 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 330
ID ADE04678 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 331
ID ADE92807 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 332
ID ADE21516 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 333
ID ADE23157 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 334
ID ADE97492 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 335
ID ADE80556 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 336
ID ADE80004 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 337
ID ADE80004 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;

Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 337
ID ADG63772 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 338
ID ADH62528 standard; protein; 299 AA.
DE Human PRO301 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 339
ID ADH59235 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 340
ID ADH55296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 341
ID ADH55848 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 342
ID ADI38014 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 343
ID ADI64067 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 344
ID ADI65016 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 345
ID ADI63515 standard; protein; 299 AA.

DE Novel human secreted and transmembrane protein PRO301.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 346
ID ADH81929 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 347
ID ADH81377 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 348
ID ADJ26282 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 349
ID ADM82546 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 350
ID ADN15945 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 351
ID ADN16574 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 352
ID ADN15393 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 353
ID ADN14841 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 354
ID ADC81103 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.

PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 355
ID ADE79197 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 356
ID ADE76551 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 357
ID ADE87915 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 358
ID ADE86319 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 359
ID ADE79621 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 360
ID ADE75767 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 361
ID ADE73297 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003128592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 362
ID ADE841304 standard; protein; 299 AA.
DE Human secreted/cranmembrane PRO polypeptide #27.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 363
ID ADE23343 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092108-A1.
PD 13-NOV-2003.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 364
ID ADE23695 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 365
ID ADE24538 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 366
ID ADE87363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 367
ID ADE89229 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 368
ID ADE841186 standard; protein; 299 AA.
DE Human secreted/cranmembrane polypeptide PRO301.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 369
ID ADE73832 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 370
ID ADE18368 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 371
ID ADE88677 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 372
ID ADE93586 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003211576-A1.
PD 13-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 373
ID ADE94697 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 374
ID ADE91108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 375
ID ADE95249 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 376
ID ADE93359 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 377
ID ADF34940 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 378
ID ADE96505 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 379
ID ADE92255 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 380
ID ADE90556 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 381
ID ADE91703 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 382
ID ADE96932 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 383
ID ADG40402 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P. J.
PA (GURN/) GURNEY A. L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 384
ID ADF73796 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 385
ID ADG02282 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 386
ID ADG22068 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 387
ID ADG20138 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 388
ID ADP98044 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 389
ID ADG24261 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 390

ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 391
ID ADG03446 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 392
ID ADF99167 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 393
ID ADG16752 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 394
ID ADG05211 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 395
ID ADG19478 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 396
ID ADF73372 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein. #25.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 397
ID ADG13315 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 398
ID ADG08372 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 399
ID ADG15542 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 400
ID ADF96940 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 401
ID ADG06125 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 402
ID ADG23709 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 403
ID ADG03998 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 404
ID ADG24899 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 405
ID ADG07196 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 406
ID ADG07748 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 407
ID ADG55243 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 408
ID ADG60907 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.

PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 409
ID ADG62011 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 410
ID ADG92215 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003207145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 411
ID ADG82212 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 412
ID ADG57451 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 413
ID ADG56899 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 414
ID ADG55795 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 415
ID ADG5555 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 416
ID ADG70921 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 417
ID ADG92642 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003207146-A1.
PA (GETH) GENENTECH INC.

PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 418
ID ADG58003 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 419
ID ADG53587 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 420
ID ADG71473 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 421
ID ADG81660 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 422
ID ADH30622 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 423
ID ADG63621 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 424
ID ADH11989 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 425
ID ADG52411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 426
ID ADG54139 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 427
ID ADG81108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 428
ID ADG56347 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 429
ID ADH12613 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 430
ID ADG61459 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 431
ID ADI28546 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 432
ID ADG54691 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 433
ID ADG59731 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 434
ID ADH20431 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 435
ID ADH43487 standard; protein; 299 AA.
DE Human PRO polypeptide #27.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 436
ID ADH07286 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOMSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 437
ID ADH59631 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 438
ID ADH06859 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOMSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 439
ID ADI18155 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 440
ID ADI18601 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 441
ID ADI65321 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 442
ID ADI37584 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 443
ID ADG09898 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004009548-A1.

[illegible]

Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 452		
ID ADL08741 standard; protein; 299 AA.		
DE Human secreted/transmembrane protein, #25.		
PN US2003186358-A1.		
PD 02-OCT-2003.		
PA (GETH) GENENTECH INC.		
Query Match	10.6%;	Score 178.5; DB 8; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 453		
ID ADI47176 standard; protein; 299 AA.		
DE Human JAM-1 protein sequence.		
PN WO2004003145-A2.		
PD 08-JAN-2004.		
PA (NAST-) NASTECH PHARM CO INC.		
Query Match	10.6%;	Score 178.5; DB 8; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 454		
ID ADM25082 standard; protein; 299 AA.		
DE Human secreted/transmembrane protein, #25.		
PN US2003096233-A1.		
PD 22-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	10.6%;	Score 178.5; DB 8; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 455		
ID ADK40844 standard; protein; 299 AA.		
DE Human platelet F11 receptor #1.		
PN US6699688-B1.		
PD 02-MAR-2004.		
PA (UTNY) UNIV NEW YORK STATE RES FOUND.		
Query Match	10.6%;	Score 178.5; DB 8; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 456		
ID ADG63577 standard; protein; 299 AA.		
DE Novel human secreted and transmembrane protein PRO301.		
PN US2004039164-A1.		
PD 26-FEB-2004.		
PA (GETH) GENENTECH INC.		
Query Match	10.6%;	Score 178.5; DB 8; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 457		
ID ADM29832 standard; protein; 299 AA.		
DE Human secreted/transmembrane protein, #25.		
PN US2003190611-A1.		
PD 09-OCT-2003.		
PA (GETH) GENENTECH INC.		
Query Match	10.6%;	Score 178.5; DB 8; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 458		
ID ADI77818 standard; protein; 299 AA.		
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1300.		
PN US2004010134-A1.		
PD 15-JAN-2004.		
PA (ROSE/) ROSEN C A.		
PA (HASE/) HASELTINE W A.		
Query Match	10.6%;	Score 178.5; DB 8; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 459		
ID ADI77819 standard; protein; 299 AA.		
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1301.		
PN US2004010134-A1.		
PD 15-JAN-2004.		
PA (ROSE/) ROSEN C A.		
PA (HASE/) HASELTINE W A.		
Query Match	10.6%;	Score 178.5; DB 8; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 460		
ID ADJ77472 standard; protein; 299 AA.		
DE Human pro polypeptide #183.		
PN US2004038336-A1.		
PD 26-FEB-2004.		
PA (GETH) GENENTECH INC.		

Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 461
ID ADM2832 standard; protein; 299 AA.
DE Human PRO polypeptide #27.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 462
ID ADM5594 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 463
ID ADJ3132 standard; protein; 299 AA.
DE Human protein encoded by a full length cDNA clone cseqID 3365.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 464
ID ADM27730 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 465
ID ADI26800 standard; protein; 299 AA.
DE Human JAM1 protein SEQ ID NO:54.
PN WO2004022778-A1.
PD 18-MAR-2004.
PA (GARV-) GARVAN INST MEDICAL RES.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 466
ID ADM42454 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 467
ID ADO06154 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 468
ID ADN35284 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 469
ID ADN05140 standard; protein; 299 AA.
DE Antipeptidic protein sequence #749.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;

Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 470
ID ADM28316 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 471
ID ADE09073 standard; protein; 320 AA.
DE Novel protein-related contig polypeptide sequence #139.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 178.5; DB 7; Length 320;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 472
ID ADJ67616 standard; protein; 335 AA.
DE Human ovarian specific polypeptide SEQ ID NO:330.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 10.6%; Score 178.5; DB 8; Length 335;
Best Local Similarity 26.5%; Pred. No. 1.2e-06;
RESULT 473
ID ADE08038 standard; protein; 336 AA.
DE Novel protein (useful for identifying genetic disorders) #193.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 178.5; DB 7; Length 336;
Best Local Similarity 26.5%; Pred. No. 1.2e-06;
RESULT 474
ID AAW14146 standard; protein; 319 AA.
DE Human A33 antigen.
PN WO9708189-A1.
PD 06-MAR-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 10.5%; Score 177; DB 2; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.5e-06;
RESULT 475
ID AAY23323 standard; protein; 319 AA.
DE Amino acid sequence of the A33 antigen.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 177; DB 2; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.5e-06;
RESULT 476
ID AAB5863 standard; protein; 319 AA.
DE Human A33 protein SEQ ID NO: 67.
PN WO200078808-A1.
PD 28-DEC-2000.
PA (MITL-) MILLENNIUM PHARM INC.
Query Match 10.5%; Score 177; DB 4; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.5e-06;
RESULT 477
ID ADA10947 standard; protein; 319 AA.
DE Human cDNA differentially expressed in colon cancer #43 product.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Query Match 10.5%; Score 177; DB 6; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.5e-06;
RESULT 478
ID ADH62533 standard; protein; 319 AA.
DE Human A33 antigenic protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.

PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.5%; Score 177; DB 7; Length 319;
Pred. No. 1.5e-06;
RESULT 479
ID ADN39847 standard; protein; 319 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C217.
PN W0200304261-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 10.5%; Score 177; DB 7; Length 319;
Pred. No. 1.5e-06;
RESULT 480
ID ADN35289 standard; protein; 319 AA.
DE Human A33 antigen protein.
PN W02004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 177; DB 8; Length 319;
Pred. No. 1.5e-06;
RESULT 481
ID ABP62881 standard; protein; 336 AA.
DE Human polypeptide SEQ ID NO 318.
PN W0200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 10.5%; Score 177; DB 5; Length 336;
Pred. No. 1.6e-06;
RESULT 482
ID ADC78439 standard; protein; 299 AA.
DE Human PRO301 protein.
PN W0200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 176.5; DB 3; Length 299;
Pred. No. 1.6e-06;
RESULT 483
ID AAY08073 standard; protein; 268 AA.
DE Human A33 protein.
PN W09914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 176; DB 2; Length 268;
Pred. No. 1.5e-06;
RESULT 484
ID ADH62551 standard; protein; 268 AA.
DE Human A33 antigenic protein fragment #1.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.4%; Score 176; DB 7; Length 268;
Pred. No. 1.5e-06;
RESULT 485
ID AAY23327 standard; protein; 270 AA.
DE An A33 related antigen sequence.
PN W09927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 176; DB 2; Length 270;
Pred. No. 1.5e-06;
RESULT 486
ID AAY23329 standard; protein; 273 AA.
DE An A33 related antigen sequence.
PN W09927098-A2.

PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 176; DB 2; Length 273;
Pred. No. 1.5e-06;
RESULT 487
ID AAY08075 standard; protein; 273 AA.
DE Human A33 protein fragment #2.
PN W09914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 176; DB 2; Length 273;
Pred. No. 1.5e-06;
RESULT 488
ID ADH62553 standard; protein; 273 AA.
DE Human A33 antigenic protein fragment #2.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.4%; Score 176; DB 7; Length 273;
Pred. No. 1.5e-06;
RESULT 489
ID ADH80722 standard; protein; 301 AA.
DE Human polypeptide #39.
PN US2003232054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOI/) CAO Y.
PA (DRMA/) DRMANAC R T.
Query Match
Best Local Similarity 10.3%; Score 173.5; DB 8; Length 301;
Pred. No. 2.8e-06;
RESULT 490
ID ADK40854 standard; protein; 316 AA.
DE Human A33 molecule.
PN US6699688-B1.
PD 02-MAR-2004.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
Query Match
Best Local Similarity 10.2%; Score 172.5; DB 8; Length 316;
Pred. No. 3.7e-06;
RESULT 491
ID AAY23326 standard; protein; 260 AA.
DE An A33 related antigen sequence.
PN W09927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.0%; Score 169.5; DB 2; Length 260;
Pred. No. 5.1e-06;
RESULT 492
ID AAY08072 standard; protein; 260 AA.
DE Human DNA40628 protein.
PN W09914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.0%; Score 169.5; DB 2; Length 260;
Pred. No. 5.1e-06;
RESULT 493
ID ADH62550 standard; protein; 260 AA.
DE Human PRO301 protein fragment #1.
PN US2003171568-A1.
PD 11-SEP-2003.

PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.0%; Score 169.5; DB 7; Length 260;
RESULT 494
ID AAY23328 standard; protein; 263 AA.
DE An A33 related antigen sequence.
PN MO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.0%; Score 169.5; DB 2; Length 263;
RESULT 495
ID AAY08074 standard; protein; 263 AA.
DE Human DNA40628 protein fragment #2.
PN MO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.0%; Score 169.5; DB 2; Length 263;
RESULT 496
ID ADH62552 standard; protein; 263 AA.
DE Human PRO301 protein fragment #2.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.0%; Score 169.5; DB 7; Length 263;
RESULT 497
ID AAW61379 standard; protein; 298 AA.
DE Human junctional adhesion molecule protein.
PN MO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match
Best Local Similarity 9.9%; Score 167; DB 2; Length 298;
RESULT 498
ID AAW61380 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule protein.
PN MO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match
Best Local Similarity 9.9%; Score 167; DB 2; Length 300;
RESULT 499
ID AAY23325 standard; protein; 300 AA.
DE A33 related antigen JAM.
PN MO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 167; DB 2; Length 300;
RESULT 500
ID ADH62537 standard; protein; 300 AA.
DE Murine JAM protein used in the exemplification of the invention.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 9.9%; Score 167; DB 5; Length 365;
RESULT 504
ID ABB83927 standard; protein; 261 AA.
DE C-terminally truncated PCAR SEQ ID NO 2.
PN US2002059654-A1.
PD 16-MAY-2002.
PA (BUHL/) BUHLER T. A.
PA (GADI/) GADIENT R A.
PA (KORN/) KORN R.
PA (MOVV/) MOVVA R.
Query Match
Best Local Similarity 9.8%; Score 166; DB 5; Length 365;
RESULT 505
ID AAM14158 standard; protein; 318 AA.
DE Mouse A33 antigen.
PN MO9708189-A1.
PD 06-MAR-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match
Best Local Similarity 9.6%; Score 162.5; DB 2; Length 318;
RESULT 506
ID AAB39253 standard; protein; 280 AA.
DE Gene 15 human secreted protein homologous amino acid sequence #133.
PN WO2000056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 9.5%; Score 160; DB 3; Length 280;
RESULT 507
ID ADA50171 standard; protein; 412 AA.
DE Human CAR/mouse SCF fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match
Best Local Similarity 9.4%; Score 158.5; DB 6; Length 412;
RESULT 508
ID AAY72878 standard; protein; 352 AA.
DE Human PRO5723 protein encoded by DNA82361 cDNA clone.
PN WO200116319-A2.

PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 4; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 509
ID AAB50930 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN W0200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 4; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 510
ID AAB65294 standard; protein; 352 AA.
DE Human PRO5723 protein sequence SEQ ID NO:505.
PN W0200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 4; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 511
ID AAB84956 standard; protein; 352 AA.
DE Human PRO5723 protein sequence SEQ ID NO:280.
PN W0200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 5; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 512
ID AAB95562 standard; protein; 352 AA.
DE Human angiogenesis related protein PRO5723 SEQ ID NO: 280.
PN W0200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERB/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOMSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATNABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 9.4%; Score 158; DB 5; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 513
ID AAB58109 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 514
ID AAB59187 standard; protein; 352 AA.
DE Novel human secreted or transmembrane protein PRO5723.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 515
ID AABU82699 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;

RESULT 516
ID AABU60618 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, #177.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 517
ID AABU80846 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 518
ID ABO33812 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 519
ID AABU14000 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 520
ID AABU72585 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 521
ID AABG74762 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN US2002192752-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 522
ID AABU59334 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, #177.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 523
ID ABO26031 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 524
ID AABU82155 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 525
ID AABU59040 standard; protein; 352 AA.

DE Human secreted/transmembrane protein, #177.
PN US2002143961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 526
ID ABU92418 standard; protein, 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 527
ID ABU59483 standard; protein, 352 AA.
DE Novel human secreted or transmembrane protein PRO3301.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 528
ID ABU92249 standard; protein, 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 529
ID ABU10955 standard; protein, 352 AA.
DE Human PRO polypeptide #141.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 530
ID ABU81707 standard; protein, 352 AA.
DE Human secreted and transmembrane protein PRO5723.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 531
ID ABU88646 standard; protein, 352 AA.
DE Human secreted and transmembrane polypeptide PRO5723.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 532
ID ABO34160 standard; protein, 352 AA.
DE Human PRO5723 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 533
ID ABU72335 standard; protein, 352 AA.
DE Human PRO5723 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 534
ID ADA38016 standard; protein, 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 535
ID ADA21702 standard; protein, 352 AA.
DE Human secreted/transmembrane polypeptide PRO5723.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 536
ID ADA10489 standard; protein, 352 AA.
DE Human secreted/transmembrane protein, PRO5723.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 537
ID ADA18033 standard; protein, 352 AA.
DE Human PRO5723 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 538
ID ADA28141 standard; protein, 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 539
ID ADA94721 standard; protein, 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 540
ID ADA38946 standard; protein, 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 541
ID ABU72463 standard; protein, 352 AA.
DE Human PRO5723 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 542
ID ADA93067 standard; protein, 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 543
ID ABO34358 standard; protein, 352 AA.
DE Human secreted/transmembrane polypeptide PRO 5723.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 544
ID ABO53246 standard; protein, 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;

RESULT 545
ID ADA22628 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO5723.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 546
ID ABO22616 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 547
ID ADA06794 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #141.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 548
ID ABU72165 standard; protein; 352 AA.
DE Human membrane bound receptor/protein PRO5723 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 549
ID ADA39487 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 550
ID ADB83706 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 551
ID ADB80812 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 552
ID ADB7353 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 553
ID ADB96513 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 554
ID ADB78435 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 555
ID ADB85083 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 556
ID ADB78189 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 557
ID ADB87255 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 558
ID ADB84837 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 559
ID ADB83952 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 560
ID ADB7107 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 561
ID ADC57985 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 562
ID ADC55349 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 563
ID ADC12216 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 564
ID ADC56638 standard; protein; 352 AA.

[illegible]

[illegible]

Best Local Similarity	23.3%	Pred. No. 7,4e-05;
RESULT 593		
ID AD54674 standard; protein; 352 AA.		
DE Human PRO polypeptide #141.		
FN US2002132253-A1.		
PD 19-SEP-2002.		
PA (GETH) GENENTECH INC.		
Query Match	9.4%	Score 158; DB 7; Length 352;
Best Local Similarity	23.3%	Pred. No. 7,4e-05;
RESULT 594		
ID AD50361 standard; protein; 352 AA.		
DE Human PRO polypeptide #108.		
FN US2003096970-A1.		
PD 22-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	9.4%	Score 158; DB 7; Length 352;
Best Local Similarity	23.3%	Pred. No. 7,4e-05;
RESULT 595		
ID AD51372 standard; protein; 352 AA.		
DE Novel human secreted and transmembrane protein PRO5723.		
FN US003105289-A1.		
PD 05-JUN-2003.		
PA (GETH) GENENTECH INC.		
Query Match	9.4%	Score 158; DB 7; Length 352;
Best Local Similarity	23.3%	Pred. No. 7,4e-05;
RESULT 596		
ID AD51893 standard; protein; 352 AA.		
DE Human secreted/transmembrane protein PRO5723.		
FN US2003068647-A1.		
PD 10-APR-2003.		
Query Match	9.4%	Score 158; DB 7; Length 352;
Best Local Similarity	23.3%	Pred. No. 7,4e-05;
RESULT 597		
ID AD527028 standard; protein; 352 AA.		
DE Novel human secreted and transmembrane protein PRO5723.		
FN US2003087304-A1.		
PD 08-MAY-2003.		
Query Match	9.4%	Score 158; DB 7; Length 352;
Best Local Similarity	23.3%	Pred. No. 7,4e-05;
RESULT 598		
ID AD526495 standard; protein; 352 AA.		
DE Novel human secreted and transmembrane protein PRO5723.		
FN US2003087305-A1.		
PD 08-MAY-2003.		
Query Match	9.4%	Score 158; DB 7; Length 352;
Best Local Similarity	23.3%	Pred. No. 7,4e-05;
RESULT 599		
ID AD567432 standard; protein; 352 AA.		
DE Human PRO5723 amino acid sequence SEQ ID NO:505.		
FN US2002198148-A1.		
PD 26-DEC-2002.		
PA (GETH) GENENTECH INC.		
Query Match	9.4%	Score 158; DB 7; Length 352;
Best Local Similarity	23.3%	Pred. No. 7,4e-05;
RESULT 600		
ID AD594085 standard; protein; 352 AA.		
DE Immune disease treatment/diagnosis related PRO5723.		
FN US2003082199-A1.		
PD 01-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	9.4%	Score 158; DB 7; Length 352;
Best Local Similarity	23.3%	Pred. No. 7,4e-05;
RESULT 601		
ID AD135686 standard; protein; 352 AA.		
DE Human PRO polypeptide #141.		
FN US2003050457-A1.		
PD 13-MAR-2003.		
Query Match	9.4%	Score 158; DB 7; Length 352;
Best Local Similarity	23.3%	Pred. No. 7,4e-05;
RESULT 602		
ID AD100179 standard; protein; 352 AA.		
DE Novel human secreted and transmembrane protein PRO5723.		
FN US2003049682-A1.		

PD 13-MAR-2003.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 603
ID ADE48919 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 604
ID ADE21090 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 605
ID ADE05934 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 606
ID ADD75163 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 607
ID ADD75909 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 608
ID ADD85141 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 609
ID ADE20598 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 610
ID ADE20844 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 611
ID ADE39141 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096362-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 612
ID ADE05688 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 613
ID ADD73673 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 614
ID ADD78513 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 615
ID ADE41530 standard; protein: 352 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 616
ID ADE21336 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 617
ID ADD77451 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 618
ID ADE20598 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 619
ID ADD75663 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 620
ID ADD74179 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;

Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 621
ID ADD74425 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 622
ID ADD76155 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 623
ID ADD85647 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 624
ID ADE05196 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 625
ID ADD75409 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 626
ID ADD76953 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 627
ID ADD86721 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 628
ID ADD78189 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 629
ID ADD77697 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;

RESULT 630
ID ADD77943 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 631
ID ADD85401 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 632
ID ADD73933 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 633
ID ADD74671 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 634
ID ADD77199 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 635
ID ADD85893 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 636
ID ADE05442 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 637
ID ADD74917 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 638
ID ADP35631 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 639
ID ADG11881 standard; protein; 352 AA.

DE Human PRO5723 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 640
ID ADG05729 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 641
ID ADG27283 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 642
ID ADG1346 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096867-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 643
ID ADG12125 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 644
ID ADP94682 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 645
ID ADG06778 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 646
ID ADH39122 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 647
ID ADH19751 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 648
ID ADH21244 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 649
ID ADH20284 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 650
ID ADH43713 standard; protein; 352 AA.
DE Human PRO polypeptide #140.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 651
ID ADG34212 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 652
ID ADI33682 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 653
ID ADH69776 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 654
ID ADI29937 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 655
ID ADW2734 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 656
ID ADK83058 standard; protein; 352 AA.
DE Human PRO polypeptide #140.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 657
ID ADK6692 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2004044180-A1.
PD 04-MAR-2004.

PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 658
ID AAW69697 standard; protein; 365 AA.
DE Human coxsackievirus and Ad2 and Ad5 receptor HCAR protein.
PN WO9833819-A1.
PD 06-AUG-1998.
PA (UYNV) UNIV NEW YORK STATE.
Query Match 9.4%; Score 158; DB 2; Length 365;
Best Local Similarity 23.3%; Pred. No. 7.8e-05;
RESULT 659
ID AAW57212 standard; protein; 365 AA.
DE Human coxsackievirus and adenovirus receptor.
PN WO9811221-A2.
PD 19-MAR-1998.
PA (DAND) DANA FARBEN CANCER INST INC.
Query Match 9.4%; Score 158; DB 2; Length 365;
Best Local Similarity 23.3%; Pred. No. 7.8e-05;
RESULT 660
ID AAB47270 standard; protein; 365 AA.
DE Human CAR.
PN US6245966-B1.
PD 12-JUN-2001.
PA (UYTE-) UNIV TECHNOLOGY CORP.
Query Match 9.4%; Score 158; DB 4; Length 365;
Best Local Similarity 23.3%; Pred. No. 7.8e-05;
RESULT 661
ID ABB08040 standard; protein; 365 AA.
DE Human coxsackie-adenovirus receptor (CAR).
PN WO200229072-A2.
PD 11-APR-2002.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERB GBS MBH.
Query Match 9.4%; Score 158; DB 5; Length 365;
Best Local Similarity 23.3%; Pred. No. 7.8e-05;
RESULT 662
ID ABJ37063 standard; protein; 365 AA.
DE Human breast cancer / ovarian cancer related protein #39.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILN-) MILLENNIUM PHARM INC.
Query Match 9.4%; Score 158; DB 6; Length 365;
Best Local Similarity 23.3%; Pred. No. 7.8e-05;
RESULT 663
ID ADB97544 standard; protein; 365 AA.
DE Human CAR wild-type protein.
PN WO2003070915-A2.
PD 28-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 9.4%; Score 158; DB 7; Length 365;
Best Local Similarity 23.3%; Pred. No. 7.8e-05;
RESULT 664
ID ADN95226 standard; protein; 365 AA.
DE Human BEC/LSC-related protein sequence SegID148.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 9.4%; Score 158; DB 7; Length 365;
Best Local Similarity 23.3%; Pred. No. 7.8e-05;
RESULT 665
ID ABU12046 standard; protein; 505 AA.
DE Human NOV4a CG59871-01 protein SEQ ID 12.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 158; DB 6; Length 505;
Best Local Similarity 23.3%; Pred. No. 0.00012;
RESULT 666
ID ADJ67617 standard; protein; 351 AA.
DE Human ovarian specific polypeptide SEQ ID NO:331.
PN WO2004013311-A2.

PD 12-FEB-2004.
PA (DIAD-) DIDEDEXUS INC.
Query Match 9.3%; Score 157.5; DB 8; Length 351;
Best Local Similarity 23.0%; Pred. No. 8.1e-05;
RESULT 667
ID ADA50172 standard; protein; 493 AA.
DE Human CAR/mouse anti-CD34 antibody fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match 9.3%; Score 157.5; DB 6; Length 493;
Best Local Similarity 23.7%; Pred. No. 0.00013;
RESULT 668
ID AAW82729 standard; protein; 264 AA.
DE Adenovirus PACTSG2-SCAR protein.
PN WO9854346-A1.
PD 03-DEC-1998.
PA (GENV-) GENVEEC INC.
Query Match 9.3%; Score 156.5; DB 2; Length 264;
Best Local Similarity 25.9%; Pred. No. 6.7e-05;
RESULT 669
ID AAW82730 standard; protein; 277 AA.
DE Adenovirus SCAR.RGD protein.
PN WO9854346-A1.
PD 03-DEC-1998.
PA (GENV-) GENVEEC INC.
Query Match 9.3%; Score 156.5; DB 2; Length 277;
Best Local Similarity 25.9%; Pred. No. 7.2e-05;
RESULT 670
ID AAU83699 standard; protein; 290 AA.
DE Human PRO protein, Seq ID No 216.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 156.5; DB 5; Length 290;
Best Local Similarity 25.9%; Pred. No. 7.7e-05;
RESULT 671
ID AAW82731 standard; protein; 397 AA.
DE Adenovirus PACSG2SCAR.slg chimeric protein.
PN WO9854346-A1.
PD 03-DEC-1998.
PA (GENV-) GENVEEC INC.
Query Match 9.3%; Score 156.5; DB 2; Length 397;
Best Local Similarity 25.9%; Pred. No. 0.00012;
RESULT 672
ID ADA50170 standard; protein; 412 AA.
DE Human CAR/SCF fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match 9.3%; Score 156.5; DB 6; Length 412;
Best Local Similarity 25.9%; Pred. No. 0.00012;
RESULT 673
ID ABG02019 standard; protein; 737 AA.
DE Novel human diagnostic protein #2010.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.2%; Score 156; DB 4; Length 737;
Best Local Similarity 24.3%; Pred. No. 0.0003;
RESULT 674
ID AAY41692 standard; protein; 373 AA.
DE Human PRO 363 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 2; Length 373;

Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 675
ID AAB33430 standard; protein; 373 AA.
DE Human PRO363 protein UNQ318 SEQ ID NO:87.
PN WO20053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 3; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 676
ID AAB4448 standard; protein; 373 AA.
DE Human PRO363 (UNQ318) protein sequence SEQ ID NO:59.
PN WO20053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 3; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 677
ID AAB12365 standard; protein; 373 AA.
DE Human PRO363 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 4; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 678
ID AAB48146 standard; protein; 373 AA.
DE Human A236 variant 2 polypeptide.
PN WO20069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 9.1%; Score 153.5; DB 4; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 679
ID AAB48108 standard; protein; 373 AA.
DE Human A236 polypeptide.
PN WO20069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 9.1%; Score 153.5; DB 4; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 680
ID AAB65293 standard; protein; 373 AA.
DE Human PRO363 protein sequence SEQ ID NO:503.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 4; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 681
ID AAB83656 standard; protein; 373 AA.
DE Human PRO protein, Seq ID No 130.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 5; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 682
ID AAB8448 standard; protein; 373 AA.
DE Human PRO363 protein sequence SEQ ID NO:64.
PN WO20020690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 5; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 683
ID AAB26448 standard; protein; 373 AA.
DE Human A236 protein.
PN US2002055139-A1.
PD 03-MAY-2002.
PA (HOLT/) HOLTZMAN D A.
PA (SHAR/) SHARP J D.
PA (LEIB/) LEIBY K R.
PA (BOSS/) BOSSONE S.
PA (PANY/) PAN Y.
PA (BARN/) BARNES T M.
PA (FRAS/) FRASER C C.
PA (WRIGHT/) WRIGHTON N.
PA (MYER/) MYERS P S.
PA (KING/) KINGSBURY G.
Query Match 9.1%; Score 153.5; DB 5; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 684
ID ABB95454 standard; protein; 373 AA.
DE Human angiogenesis related protein PRO363 SEQ ID NO: 64.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOBSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 9.1%; Score 153.5; DB 5; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 685
ID ABB58108 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 686
ID ABB59186 standard; protein; 373 AA.
DE Novel human secreted or transmembrane protein PRO363.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 687
ID ABB82698 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003034023-A1.
PD 13-FEB-2003.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 688
ID ABB017609 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 689
ID ABB060617 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, #176.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 690
ID ABB080803 standard; protein; 373 AA.
DE Human PRO polypeptide #65.

PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 691
ID ABO25194 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 692
ID ABO33769 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 693
ID ABU13999 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 694
ID ABU81063 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 695
ID ABU72200 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2002127206-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 696
ID ABU72584 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 697
ID ABU66763 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 698
ID ABU84880 standard; protein; 373 AA.
DE Human secreted and transmembrane polypeptide PRO363.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 699
ID ABU59844 standard; protein; 373 AA.
DE Novel secreted and transmembrane protein PRO363.
PN US2003017563-A1.

PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 700
ID ABU61078 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 701
ID ABU59333 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, #176.
PN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 702
ID ABO26030 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 703
ID ABO25034 standard; protein; 373 AA.
DE Human secreted/transmembrane protein (PRO) #194.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 704
ID ABU80347 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 705
ID ABU82112 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 706
ID ABU59039 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, #176.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 707
ID ABU92417 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 708
ID ABU59482 standard; protein; 373 AA.
DE Novel human secreted or transmembrane protein PRO5723.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;

```
RESULT 709
ID ABU67039 standard; protein; 373 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 388.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 710
ID ABU92248 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 711
ID ABU10954 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 712
ID ABU81706 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 713
ID ABU88645 standard; protein; 373 AA.
DE Human secreted and transmembrane polypeptide PRO363.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 714
ID ABO34159 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 715
ID ADA45907 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 716
ID ADA76338 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 717
ID ABU72292 standard; protein; 373 AA.
DE Human PRO363 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 718
ID ADA18988 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 719
ID ADA61611 standard; protein; 373 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 720
ID ADA19396 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 721
ID ADB27937 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 722
ID ADA86416 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 723
ID ADB15980 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 724
ID ADA38014 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 725
ID ADA47766 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 726
ID ADA21700 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO363.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 727
ID ADA10487 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 728
ID ADA10487 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003059831-A1.
PD 27-MAR-2003.
```

Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 728
ID ADA67561 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 729
ID ADB30568 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 730
ID ADA85864 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 731
ID ADA18031 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 732
ID ADA97076 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 733
ID ADA79380 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 734
ID ADA87519 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 735
ID ADB16721 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 736
ID ADA28139 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 737

ID ADA91813 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 738
ID ADB14876 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 739
ID ADA24598 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 740
ID ADB18837 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 741
ID ADA94052 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 742
ID ADB19948 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 743
ID ADB13260 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 744
ID ABO43342 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 745
ID ABO19649 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 6; Length 373;
RESULT 746
ID ADA12259 standard; protein; 373 AA.

DE	Human secreted/transmembrane polypeptide PRO363.
PN	US2003055216-A1.
PD	20-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 747	
ID	ADA94719 standard; protein: 373 AA.
DE	Human secreted/transmembrane protein PRO363.
PN	US2003059832-A1.
PD	27-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 748	
ID	ADA74514 standard; protein: 373 AA.
DE	Human PRO polypeptide #194.
PN	US2003068798-A1.
PD	10-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 749	
ID	ADB24747 standard; protein: 373 AA.
DE	Human PRO polypeptide SEQ ID NO 388.
PN	US2003077713-A1.
PD	24-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 750	
ID	ADA82271 standard; protein: 373 AA.
DE	Human PRO polypeptide #194.
PN	US2003082701-A1.
PD	01-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 751	
ID	ADA75234 standard; protein: 373 AA.
DE	Human PRO polypeptide #194.
PN	US2003073216-A1.
PD	17-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 752	
ID	ADA85312 standard; protein: 373 AA.
DE	Novel human secreted and transmembrane protein PRO363.
PN	US2003082695-A1.
PD	01-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 753	
ID	ADA84760 standard; protein: 373 AA.
DE	Novel human secreted and transmembrane protein PRO363.
PN	US2003082708-A1.
PD	01-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 754	
ID	ADB30016 standard; protein: 373 AA.
DE	Human PRO polypeptide #194.
PN	US2003073214-A1.
PD	17-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 755	
ID	ADA80544 standard; protein: 373 AA.
DE	Human PRO polypeptide #194.
PN	US2003082761-A1.
PD	27-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 756	
ID	ADAB2683 standard; protein: 373 AA.
DE	Human PRO polypeptide #194.
PN	US2003092147-A1.
PD	15-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 761	
ID	ADAB31120 standard; protein: 373 AA.
DE	Human PRO polypeptide #194.
PN	US2003096386-A1.
PD	22-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 762	
ID	ADAB72420 standard; protein: 373 AA.
DE	Human PRO363 protein.
PN	US2003027988-A1.
PD	06-FEB-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 764	
ID	ADA93065 standard; protein: 373 AA.
DE	Human secreted/transmembrane protein PRO363.
PN	US2003060407-A1.
PD	27-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 765	
ID	ADAB2683 standard; protein: 373 AA.
DE	Human PRO polypeptide #194.
PN	US2003077715-A1.
PD	24-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 759	
ID	ADB25307 standard; protein: 373 AA.
DE	Human PRO polypeptide SEQ ID NO 388.
PN	US2003077715-A1.
PD	24-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 759	
ID	ADB25307 standard; protein: 373 AA.
DE	Human PRO polypeptide SEQ ID NO 388.
PN	US2003077715-A1.
PD	24-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 760	
ID	ADA93483 standard; protein: 373 AA.
DE	Human PRO polypeptide #194.
PN	US2003077721-A1.
PD	24-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 761	
ID	ADAB2683 standard; protein: 373 AA.
DE	Human PRO polypeptide #194.
PN	US2003092147-A1.
PD	15-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	9.1%; Score 153.5; DB 6;
Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 762	
ID	ADAB31120 standard; protein: 373 AA.
DE	Human PRO polypeptide #194.
PN	US2003096386-A1.

Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 765
ID ADA61048 standard; protein; 373 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 766
ID ADB24195 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 767
ID ADA96524 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 768
ID ADA81096 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 769
ID ADA95972 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 770
ID ADB26281 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 771
ID ADB21766 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 772
ID ABO34315 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO 363.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 773
ID ABO19540 standard; protein; 373 AA.
DE Novel human secreted and transmembrane polypeptide #8.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 774

ID ADA77545 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 775
ID ADB18285 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 776
ID ADA86968 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 777
ID ADA88071 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 778
ID ADA46459 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 779
ID ADB28489 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 780
ID ADB29041 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 781
ID ABO53245 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 782
ID ADA76993 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 783
ID ADA22626 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO363.

PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 784
ID ADB8623 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073213-A1.
PD 17-APR-2003.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 785
ID ADB97628 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 786
ID ADB27385 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 787
ID ADB22318 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 788
ID ABO22615 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 789
ID ADB06792 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 790
ID ABO72122 standard; protein; 373 AA.
DE Human membrane bound receptor/protein PRO363 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 791
ID ADA39485 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 792
ID ADA67009 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 793
ID ADB2870 standard; protein; 373 AA.

DE Human PRO polypeptide #194.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 794
ID ADB23643 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 795
ID ADA92365 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 796
ID ADB15428 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 797
ID ADB83620 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 798
ID ADB80726 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 799
ID ADB73267 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US200306968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 800
ID ADB3680 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 801
ID ADB96511 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 802
ID ADB78349 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092889-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 803
ID ADB3128 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 804
ID ADB6660 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 805
ID ADB84997 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 806
ID ADB89680 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 807
ID ADB90412 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 808
ID ADB39513 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 809
ID ADB78103 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 810
ID ADB73565 standard; protein; 373 AA.
DE Human PRO polypeptide #8.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 811
ID ADB87169 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003088067-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 812
ID ADB84751 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 813
ID ADB47136 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 814
ID ADB83866 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 815
ID ADB86743 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 816
ID ADB73021 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 817
ID ADB76281 standard; protein; 373 AA.
DE Human PRO polypeptide #8.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 818
ID ADB77348 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 819
ID ADB34505 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 820
ID ADB35609 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 821
ID ADB33953 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 822
ID ADB35057 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 823
ID ADB36161 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 824
ID ADB46556 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 825
ID ADC43707 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 826
ID ADC57983 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 827
ID ADC55347 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 828
ID ADC12214 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 829
ID ADC61467 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 830
ID ADC63431 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 831
ID ADC66531 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 832
ID ADC56636 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 833
ID ADC68655 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 834
ID ADC62715 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 835
ID ADC67780 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 836
ID ADC11681 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003058403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 837
ID ADC41100 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 838
ID ADC67155 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 839
ID ADC62091 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003073624-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 840
ID ADC36859 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 841
ID ADC41724 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 842
ID ADC21849 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 843
ID ADC59429 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 844
ID ADC71976 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 845
ID ADC59955 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 846
ID ADC49880 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 847
ID ADC45079 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 848
ID ADC4596 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;

Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 849
ID ADC47457 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 850
ID ADC52962 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 851
ID ADC57316 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 852
ID ADC6507 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 853
ID ADC50982 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 854
ID ADC65509 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 855
ID ADC54607 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 856
ID ADC53568 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 857
ID ADC59091 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;

Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 858
ID ADC55969 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein Seg ID388.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 859
ID ADC58539 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein Seg ID388.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 860
ID ADC14603 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 861
ID ADC47202 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 862
ID ADD08335 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 863
ID ADD03213 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030923104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 864
ID ADC90205 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 865
ID ADC82160 standard; protein: 373 AA.
DE Human PRO polypeptide #140.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 866
ID ADC69624 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 867
ID ADC48513 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 868
ID ADD10042 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 869
ID ADD07802 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 870
ID ADC78077 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 871
ID ADD04617 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 872
ID ADC82693 standard; protein: 373 AA.
DE Human PRO polypeptide #140.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 873
ID ADD06312 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 874
ID ADC80573 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 875
ID ADD11080 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 876
ID ADD10353 standard; protein: 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003105011-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 877
ID ADC47961 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 878
ID ADD08873 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 879
ID ADC77831 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 880
ID ADC80021 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 881
ID ADD07122 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 882
ID ADD11313 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 883
ID ADD09490 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 884
ID ADC83369 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 885
ID ADD50794 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 886

RESULT 886
ID ADD41203 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 887
ID ADD52342 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 888
ID ADD51040 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 889
ID ADD53082 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 890
ID ADD5634 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 891
ID ADD55476 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 892
ID ADD37106 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 893
ID ADD56434 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 894
ID ADD51790 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019; Length 373;
RESULT 895
ID ADD02589 standard; protein; 373 AA.
DE Human PRO polypeptide #194.

P	N	US2003203431-A1.
PD	30-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%; Score 153.5; DB 7;	Length 373;
ID	Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 896		
ID	ADDS05521 standard; protein; 373 AA.	
DE	Human PRO polypeptide #65.	
PN	US2003096971-A1.	
PD	22-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%; Score 153.5; DB 7;	Length 373;
ID	Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 897		
ID	ADD02023 standard; protein; 373 AA.	
DE	Human PRO polypeptide #194.	
PN	US2003203430-A1.	
PD	30-OCT-2003	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%; Score 153.5; DB 7;	Length 373;
ID	Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 898		
ID	ADDS4205 standard; protein; 373 AA.	
DE	Noval human secreted and transmembrane protein PRO363.	
PN	US2003203432-A1.	
PD	30-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%; Score 153.5; DB 7;	Length 373;
ID	Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 899		
ID	ADD54872 standard; protein; 373 AA.	
DE	Human PRO polypeptide #140.	
PN	US2002132253-A1.	
PD	19-SEP-2002.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%; Score 153.5; DB 7;	Length 373;
ID	Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 900		
ID	ADDS0275 standard; protein; 373 AA.	
DE	Human PRO polypeptide #65.	
PN	US2003096970-A1.	
PD	22-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%; Score 153.5; DB 7;	Length 373;
ID	Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 901		
ID	ADD51286 standard; protein; 373 AA.	
DE	Novel human secreted and transmembrane protein PRO363.	
PN	US2003105289-A1.	
PD	05-JUN-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%; Score 153.5; DB 7;	Length 373;
ID	Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 902		
ID	ADDE49093 standard; protein; 373 AA.	
DE	Human secreted/transmembrane protein, PRO363.	
PN	US2003096744-A1.	
PD	22-MAY-2003	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%; Score 153.5; DB 7;	Length 373;
ID	Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 903		
ID	ADD92522 standard; protein; 373 AA.	
DE	Human PRO polypeptide #194.	
PN	US2003199030-A1.	
PD	23-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%; Score 153.5; DB 7;	Length 373;
ID	Best Local Similarity	27.0%; Pred. No. 0.00019;
RESULT 904		
ID	ADD91418 standard; protein; 373 AA.	
DE	Human PRO polypeptide #194.	
PN	US2003199055-A1.	

[illegible]

Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 914		
ID	AD842021 standard; protein; 373 AA.	
DE	Human PRO polypeptide #194.	
FN	US2003194772-A1.	
PD	16-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 7;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 915		
ID	AD817838 standard; protein; 373 AA.	
DE	Human PRO polypeptide #194.	
FN	US2003199023-A1.	
PD	23-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 7;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 916		
ID	ADD91970 standard; protein; 373 AA.	
DE	Human PRO polypeptide #194.	
FN	US2003199053-A1.	
PD	23-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 7;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 917		
ID	AD833433 standard; protein; 373 AA.	
DE	Novel human secreted and transmembrane protein PRO363.	
FN	US2003194767-A1.	
PD	16-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 7;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 918		
ID	AD833965 standard; protein; 373 AA.	
DE	Novel human secreted and transmembrane protein PRO363.	
FN	US2003194791-A1.	
PD	16-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 7;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 919		
ID	ADD80037 standard; protein; 373 AA.	
DE	Human PRO polypeptide #194.	
FN	US2003207417-A1.	
PD	06-NOV-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 7;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 920		
ID	ADD93074 standard; protein; 373 AA.	
DE	Human PRO polypeptide #194.	
FN	US2003194768-A1.	
PD	16-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 7;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 921		
ID	ADD72234 standard; protein; 373 AA.	
DE	Human secreted/transmembrane protein, PRO363.	
FN	US2003194781-A1.	
PD	16-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 7;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 922		
ID	AD819494 standard; protein; 373 AA.	
DE	Human PRO polypeptide #194.	
FN	US2003199025-A1.	
PD	23-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 7;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 923		
ID	AD819494 standard; protein; 373 AA.	
DE	Human PRO polypeptide #194.	
FN	US2003199025-A1.	
PD	23-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 7;
Best Local Similarity	27.0%;	Pred. No. 0.00019;

RESULT 923	ID	ADBE18942 standard; protein; 373 AA.
DE	ADBE18942 standard; protein; 373 AA.	Human PRO polypeptide #194.
PN	US2003199026-A1.	
PD	23-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		9.1%; Score 153.5; DB 7;
Best Local Similarity		27.0%; Pred. No. 0.00019;
RESULT 924	ID	ADBE43138 standard; protein; 373 AA.
DE	ADBE43138 standard; protein; 373 AA.	Human PRO polypeptide #194.
PN	US2003199033-A1.	
PD	23-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		9.1%; Score 153.5; DB 7;
Best Local Similarity		27.0%; Pred. No. 0.00019;
RESULT 925	ID	ADDP59927 standard; protein; 373 AA.
DE	ADDP59927 standard; protein; 373 AA.	Human PRO polypeptide #194.
PN	US2003199059-A1.	
PD	23-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		9.1%; Score 153.5; DB 7;
Best Local Similarity		27.0%; Pred. No. 0.00019;
RESULT 926	ID	ADBE22813 standard; protein; 373 AA.
DE	ADBE22813 standard; protein; 373 AA.	Human PRO polypeptide #194.
PN	US2003199064-A1.	
PD	23-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		9.1%; Score 153.5; DB 7;
Best Local Similarity		27.0%; Pred. No. 0.00019;
RESULT 927	ID	ADDT78931 standard; protein; 373 AA.
DE	ADDT78931 standard; protein; 373 AA.	Human PRO polypeptide #194.
PN	US2003203429-A1.	
PD	30-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		9.1%; Score 153.5; DB 7;
Best Local Similarity		27.0%; Pred. No. 0.00019;
RESULT 928	ID	ADBE26493 standard; protein; 373 AA.
DE	ADBE26493 standard; protein; 373 AA.	Novel human secreted and transmembrane protein PRO363.
PN	US2003087305-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		9.1%; Score 153.5; DB 7;
Best Local Similarity		27.0%; Pred. No. 0.00019;
RESULT 929	ID	ADBE32861 standard; protein; 373 AA.
DE	ADBE32861 standard; protein; 373 AA.	Novel human secreted and transmembrane protein PRO363.
PN	US2003194766-A1.	
PD	16-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		9.1%; Score 153.5; DB 7;
Best Local Similarity		27.0%; Pred. No. 0.00019;
RESULT 930	ID	ADBE42573 standard; protein; 373 AA.
DE	ADBE42573 standard; protein; 373 AA.	Human PRO polypeptide #194.
PN	US2003199032-A1.	
PD	23-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		9.1%; Score 153.5; DB 7;
Best Local Similarity		27.0%; Pred. No. 0.00019;
RESULT 931	ID	ADBE16885 standard; protein; 373 AA.
DE	ADBE16885 standard; protein; 373 AA.	Human secreted/transmembrane protein, PRO363.
PN	US2003203433-A1.	
PD	30-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		9.1%; Score 153.5; DB 7;
Best Local Similarity		27.0%; Pred. No. 0.00019;
RESULT 932	ID	ADBD0589 standard; protein; 373 AA.

DE Human PRO polypeptide #194.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 933.
ID ADD89617 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 934.
ID ADE40901 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 935.
ID ADE04700 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 936.
ID ADE92829 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 937.
ID ADP46899 standard; protein: 373 AA.
DE Human secreted/cranemembrane protein, PRO363.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 938.
ID ADP67430 standard; protein: 373 AA.
DE Human PRO363 amino acid sequence SEQ ID NO:503.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 939.
ID ADG21538 standard; protein: 373 AA.
DE Novel human secreted and cranemembrane protein PRO363.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 940.
ID ADG23179 standard; protein: 373 AA.
DE Novel human secreted and cranemembrane protein PRO363.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 941.
ID ADP97514 standard; protein: 373 AA.
DE Human PRO polypeptide #194.

PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 942.
ID ADG80578 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 943.
ID ADG52656 standard; protein: 373 AA.
DE Human secreted/cranemembrane protein, PRO363.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 944.
ID ADG59976 standard; protein: 373 AA.
DE Human secreted/cranemembrane protein, PRO363.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 945.
ID ADG80026 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 946.
ID ADH5318 standard; protein: 373 AA.
DE Novel human secreted and cranemembrane protein PRO363.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 947.
ID ADH58670 standard; protein: 373 AA.
DE Novel human secreted and cranemembrane protein PRO363.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 948.
ID ADI35684 standard; protein: 373 AA.
DE Human PRO polypeptide #140.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 949.
ID ADI60736 standard; protein: 373 AA.
DE Human secreted/cranemembrane protein, PRO363.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 950.
ID ADI64089 standard; protein: 373 AA.
DE Novel human secreted and cranemembrane protein PRO363.
PN US2003207385-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 951
ID ADI65038 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 952
ID ADI63537 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 953
ID ADH81951 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 954
ID ADI00177 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 955
ID ADH81399 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 956
ID ADM82568 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 957
ID ADNI15967 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 958
ID ADNI15596 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 959
ID ADNI15415 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;

Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 960
ID ADNI14863 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 961
ID ADC4833 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 962
ID ADC81125 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 963
ID ADE21004 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 964
ID ADE05848 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 965
ID ADD76573 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003100067-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 966
ID ADD75077 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 967
ID ADD75823 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 968
ID ADD85055 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;


```
RESULT 969
ID ADD86881 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 970
ID ADE20758 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100734-A1.
PD 28-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 971
ID ADE39055 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 972
ID ADE87937 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 973
ID ADD86341 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 974
ID ADE05602 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 975
ID ADD73587 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 976
ID ADE75789 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 977
ID ADE48393 standard; protein; 373 AA.
DE Human secreted/transmembrane protein. PRO363.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 978
ID ADD76427 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 979
ID ADE41314 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 980
ID ADE23365 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 981
ID ADE21250 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 982
ID ADD77365 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 983
ID ADE20512 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 984
ID ADD75577 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 985
ID ADD74093 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 986
ID ADD74339 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 987
ID ADD76069 standard; protein; 373 AA.
```

DE Novel human secreted and transmembrane protein PRO363.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 988
ID ADD85561 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 989
ID ADE23917 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 990
ID ADE24560 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 991
ID ADD87385 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 992
ID ADE05110 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 993
ID ADD75323 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 994
ID ADD76867 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 995
ID ADDE6635 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 996
ID ADE89251 standard; protein; 373 AA.
DE Human PRO polypeptide #194.

PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 997
ID ADD78103 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 998
ID ADE18390 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 999
ID ADE88699 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1000
ID ADE89494 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003130181-A1.
PD 10-UTL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERP/) GERRTSEN M B.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUDS/) KUD S S.
PA (NAPJ/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1001
ID ADD77611 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1002
ID ADD77857 standard; protein; 373 AA.

DE Novel human secreted and transmembrane protein PRO363.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1003
ID ADD85315 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1004
ID ADD73847 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1005
ID ADD74585 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1006
ID ADD77113 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1007
ID ADD85807 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1008
ID ADD85356 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1009
ID ADD74631 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1010
ID ADD61134 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1011
ID ADF39826 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1012
ID ADF45622 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1013
ID ADE94719 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1014
ID ADE91130 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1015
ID ADE35629 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1016
ID ADE95271 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1017
ID ADE93381 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1018
ID ADE24018 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1019
ID ADF40450 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1020
ID ADF23394 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203402-A1.
PD 30-OCT-2003.

PA	(GETH) GENENTECH INC.	9.1%;	Score 153.5; DB 8;	Length 373;
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1021				
ID	ADP33377 standard; protein, 373 AA.			
DE	Human secreted/transmembrane protein, PRO363.			
PN	US2003194780-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1022				
ID	ADP34362 standard; protein, 373 AA.			
DE	Human secreted/transmembrane protein, PRO363.			
PN	US2003199029-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1023				
ID	ADP26464 standard; protein, 373 AA.			
DE	Human secreted/transmembrane protein, PRO363.			
PN	US2003199436-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1024				
ID	ADP27480 standard; protein, 373 AA.			
DE	Human secreted/transmembrane protein, PRO363.			
PN	US2003199437-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1025				
ID	ADP92277 standard; protein, 373 AA.			
DE	Novel human secreted and transmembrane protein PRO363.			
PN	US2003199051-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1026				
ID	ADP90578 standard; protein, 373 AA.			
DE	Human PRO polypeptide #194.			
PN	US2003199063-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1027				
ID	ADP41074 standard; protein, 373 AA.			
DE	Human secreted/transmembrane protein, PRO363.			
PN	US2003199435-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1028				
ID	ADP32753 standard; protein, 373 AA.			
DE	Human secreted/transmembrane protein, PRO363.			
PN	US2003211091-A1.			
PD	13-NOV-2003.			
PA	(GETH) GENENTECH INC.			
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1029				
ID	ADP25119 standard; protein, 373 AA.			
DE	Human secreted/transmembrane protein, PRO363.			
PN	US2003211092-A1.			
PD	13-NOV-2003.			
PA	(GETH) GENENTECH INC.			
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1030				
ID	ADP25119 standard; protein, 373 AA.			
DE	Human secreted/transmembrane protein, PRO363.			
PN	US2003211092-A1.			
PD	13-NOV-2003.			
PA	(GETH) GENENTECH INC.			
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1031				
ID	ADP34009 standard; protein, 373 AA.			
DE	Human secreted/transmembrane protein, PRO363.			
PN	US2003194410-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1032				
ID	ADP46246 standard; protein, 373 AA.			
DE	Human secreted/transmembrane protein, PRO363.			
PN	US2003195344-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1033				
ID	ADP91725 standard; protein, 373 AA.			
DE	Novel human secreted and transmembrane protein PRO363.			
PN	US2003199058-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1034				
ID	ADG11879 standard; protein, 373 AA.			
DE	Human PRO363 polypeptide.			

```
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1039
ID ADG20160 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1040
ID ADF98066 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1041
ID ADG24283 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1042
ID ADF98637 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1043
ID ADG03468 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1044
ID ADF99189 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1045
ID ADG16774 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1046
ID ADG05233 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1047
ID ADG19500 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1048
ID ADG11260 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1049
ID ADG13337 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1050
ID ADG08394 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1051
ID ADG15564 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1052
ID ADG12039 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1053
ID ADF96962 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1054
ID ADG06147 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1055
ID ADG23731 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1056
ID ADG04020 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1057
```

ID ADG24921 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1058
ID ADF94596 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1059
ID ADG07218 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1060
ID ADG07770 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1061
ID ADG06692 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1062
ID ADG55265 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1063
ID ADG60929 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1064
ID ADG62033 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1065
ID ADG82234 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1066
ID ADG57473 standard; protein; 373 AA.

DE Novel human secreted and transmembrane protein PRO363.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1067
ID ADG56921 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1068
ID ADG55817 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1069
ID ADG58577 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1070
ID ADG70943 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1071
ID ADH39036 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1072
ID ADG58025 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1073
ID ADG53609 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1074
ID ADG71495 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1075
ID ADG50232 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.

```

PA US2003207803-A1.
PD 06-NOV-2003.
Query Match
PA (GETH ) GENENTECH INC.
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 373;
RESULT 1076 Pred. No. 0.00019;
ID ADG81682 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match
PA (GETH ) GENENTECH INC.
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 373;
RESULT 1077 Pred. No. 0.00019;
ID ADH19749 standard; protein: 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003228656-A1.
PD 11-DEC-2003.
Query Match
PA (GETH ) GENENTECH INC.
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 373;
RESULT 1078 Pred. No. 0.00019;
ID ADH30644 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003077723-A1.
PD 24-APR-2003.
Query Match
PA (GETH ) GENENTECH INC.
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 373;
RESULT 1079 Pred. No. 0.00019;
ID ADH12011 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207419-A1.
PD 06-NOV-2003.
Query Match
PA (GETH ) GENENTECH INC.
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 373;
RESULT 1080 Pred. No. 0.00019;
ID ADG49608 standard; protein: 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003215905-A1.
PD 20-NOV-2003.
Query Match
PA (GETH ) GENENTECH INC.
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 373;
RESULT 1081 Pred. No. 0.00019;
ID ADG51480 standard; protein: 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003215908-A1.
PD 20-NOV-2003.
Query Match
PA (GETH ) GENENTECH INC.
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 373;
RESULT 1082 Pred. No. 0.00019;
ID ADG52433 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207414-A1.
PD 06-NOV-2003.
Query Match
PA (GETH ) GENENTECH INC.
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 373;
RESULT 1083 Pred. No. 0.00019;
ID ADG54161 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207416-A1.
PD 06-NOV-2003.
Query Match
PA (GETH ) GENENTECH INC.
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 373;
RESULT 1084 Pred. No. 0.00019;
ID ADG48984 standard; protein: 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003216305-A1.
PD 20-NOV-2003.

```

```
PA (GETH ) GENENTECH INC.          9.1%; Score 153.5; DB 8; Length 373;
Query Match                          27.0%; Pred. No. 0.00019;
RESULT 1085
ID ADG61130 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.          9.1%; Score 153.5; DB 8; Length 373;
Query Match                          27.0%; Pred. No. 0.00019;
RESULT 1086
ID ADG6369 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.          9.1%; Score 153.5; DB 8; Length 373;
Query Match                          27.0%; Pred. No. 0.00019;
RESULT 1087
ID ADH12635 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.          9.1%; Score 153.5; DB 8; Length 373;
Query Match                          27.0%; Pred. No. 0.00019;
RESULT 1088
ID ADG48360 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.          9.1%; Score 153.5; DB 8; Length 373;
Query Match                          27.0%; Pred. No. 0.00019;
RESULT 1089
ID ADH1242 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match                          9.1%; Score 153.5; DB 8; Length 373;
Beet Local Similarity                27.0%; Pred. No. 0.00019;
RESULT 1090
ID ADG61481 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.          9.1%; Score 153.5; DB 8; Length 373;
Query Match                          27.0%; Pred. No. 0.00019;
Beet Local Similarity                27.0%; Pred. No. 0.00019;
RESULT 1091
ID ADH20282 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.          9.1%; Score 153.5; DB 8; Length 373;
Query Match                          27.0%; Pred. No. 0.00019;
Beet Local Similarity                27.0%; Pred. No. 0.00019;
RESULT 1092
ID ADH28568 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.          9.1%; Score 153.5; DB 8; Length 373;
Query Match                          27.0%; Pred. No. 0.00019;
Beet Local Similarity                27.0%; Pred. No. 0.00019;
RESULT 1093
ID ADG54713 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003020767-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.          9.1%; Score 153.5; DB 8; Length 373;
Query Match                          27.0%; Pred. No. 0.00019;
```

Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1094
ID ADG59753 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1095
ID ADG50856 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1096
ID ADH43497 standard; protein; 373 AA.
DE Human PRO polypeptide #32.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1097
ID ADG58800 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1098
ID ADG34126 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1099
ID ADG62256 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1100
ID ADI181177 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1101
ID ADI33596 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1102
ID ADH69690 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;

RESULT 1103
ID ADH25281 standard; protein; 373 AA.
DE Human neurotrophin homologue related protein sequence SEQ ID NO:59.
PN EPI386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1104
ID ADG09920 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1105
ID ADI15391 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1106
ID ADG09268 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1107
ID ADI14723 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1108
ID ADI29851 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1109
ID ADI18318 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1110
ID ADM27248 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US200404179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1111
ID ADJ63599 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1112

ID ADJ77494 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1113
ID ADK82842 standard; protein: 373 AA.
DE Human PRO polypeptide #32.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1114
ID ADK6606 standard; protein: 373 AA.
DE Human PRO polypeptide #65.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1115
ID ADJ65616 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1116
ID ADM27752 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1117
ID ADM17058 standard; protein: 373 AA.
DE Human secreted/cranmembrane protein, PRO363.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1118
ID ADJ06892 standard; protein: 373 AA.
DE Human secreted/cranmembrane protein, PRO363.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1119
ID ADM42476 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1120
ID ADN05373 standard; protein: 373 AA.
DE Antiposrotic protein sequence #858.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1121
ID ADM28338 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1122
ID ADO36720 standard; protein: 373 AA.
DE Human UKM polypeptide, SEQ ID NO:2.
PN EP1416279-A1.
PD 06-MAY-2004.
PA (HOPE) HOFFMANN LA ROCHE & CO AG F.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1123
ID ADA54925 standard; protein: 512 AA.
DE Human protein, SEQ ID 2493.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.1%; Score 153.5; DB 6; Length 512;
Best Local Similarity 25.2%; Pred. No. 0.0003;
RESULT 1124
ID AAY5366 standard; protein: 4412 AA.
DE Sequence gi/1017427/emb/CAA62189 from an alignment with protein 608.
PN WO9960164-A1.
PD 25-NOV-1999.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 9.1%; Score 153.5; DB 3; Length 4412;
Best Local Similarity 22.0%; Pred. No. 0.0055;
RESULT 1125
ID ABB60991 standard; protein: 5635 AA.
DE Novel human protein. SEQ ID 78.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 9.1%; Score 153.5; DB 5; Length 5635;
Best Local Similarity 25.2%; Pred. No. 0.0077;
RESULT 1126
ID ADJ70089 standard; protein: 5636 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1895.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 9.1%; Score 153.5; DB 7; Length 5636;
Best Local Similarity 25.2%; Pred. No. 0.0077;
RESULT 1127
ID ADJ83137 standard; protein: 5636 AA.
DE Human hemectin protein - SEQ ID 128.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT) SPYTEK K A.
PA (ZERR/) ZERHUSEN B D.
PA (PATR/) PATURAJAN M.
PA (LEPL/) LEPLLEY D M.
PA (BURG/) BURGESS C B.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSS W M.
PA (SZEK/) SZEKERS E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASH/) CASHMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLI E A.
PA (FERN/) FERNANDES E R.

```
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 7; Length 5636;
RESULT 1128
ID ADK60205 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 5636;
RESULT 1129
ID ADK60506 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 5636;
RESULT 1130
ID ADP73129 standard; protein; 5636 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P29.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 5636;
RESULT 1131
ID ADA50158 standard; protein; 393 AA.
DE Human CAR/mouse SCF mature fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match
Best Local Similarity 9.1%; Score 153; DB 6; Length 393;
RESULT 1132
ID ABG74786 standard; protein; 31267 AA.
DE Human RGS11 protein.
PN WO2002103355-A1.
PD 27-DEC-2002.
PA (TAKE/) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 9.1%; Score 153; DB 6; Length 31267;
RESULT 1133
ID ADA50159 standard; protein; 474 AA.
DE Human CAR/mouse anti-CD34 antibody mature fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match
Best Local Similarity 9.0%; Score 152; DB 6; Length 474;
RESULT 1134
ID AAB48145 standard; protein; 373 AA.
DE Human A236 variant 1 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.

PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match
Best Local Similarity 9.0%; Score 151.5; DB 4; Length 373;
RESULT 1135
ID AAU17996 standard; protein; 301 AA.
DE Human immunoglobulin polypeptide SEQ ID No 141.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 8.9%; Score 151; DB 4; Length 301;
RESULT 1136
ID ABB10232 standard; protein; 301 AA.
DE Human CDNA SEQ ID NO: 540.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 8.9%; Score 151; DB 4; Length 301;
RESULT 1137
ID ABP66819 standard; protein; 301 AA.
DE Human polypeptide SEQ ID NO 540.
PN US2002090872-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 8.9%; Score 151; DB 5; Length 301;
RESULT 1138
ID ADB31620 standard; protein; 301 AA.
DE Human novel protein SEQ ID NO 141.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 8.9%; Score 151; DB 7; Length 301;
RESULT 1139
ID ADA50157 standard; protein; 393 AA.
DE Human CAR/SCF mature fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match
Best Local Similarity 8.9%; Score 151; DB 6; Length 393;
RESULT 1140
ID ABG02117 standard; protein; 434 AA.
DE Novel human diagnostic protein #2108.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 8.9%; Score 151; DB 4; Length 434;
RESULT 1141
ID ABU62399 standard; protein; 466 AA.
DE Chimeric CAR/Hg/Pro-A gene product.
PN US6524572-B1.
PD 25-FEB-2003.
PA (RAIN-) RAINBOW THERAPEUTIC CO.
Query Match
Best Local Similarity 8.9%; Score 151; DB 6; Length 466;
RESULT 1142
ID AAB48147 standard; protein; 373 AA.
DE Human A236 variant 3 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 8.9%; Score 150.5; DB 4; Length 373;
RESULT 1143
ID ABG31321 standard; protein; 2652 AA.
```

```
DE Predicted human adlcan-2 protein.
PN W0200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 8.7%; Score 147.5; DB 5; Length 2652;
Best Local Similarity 21.8%; Pred. No. 0.009;
ID ADL02250 standard; protein; 2652 AA.
DE Human OCP protein #6.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 8.7%; Score 147.5; DB 8; Length 2652;
Best Local Similarity 21.8%; Pred. No. 0.009;
ID ABB70049 standard; protein; 2845 AA.
DE Human NOV1A.
PN W0200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.7%; Score 147.5; DB 5; Length 2845;
Best Local Similarity 21.8%; Pred. No. 0.0099;
ID ABB22401 standard; protein; 361 AA.
DE Novel human diagnostic protein #22392.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.7%; Score 146.5; DB 4; Length 361;
Best Local Similarity 24.5%; Pred. No. 0.00074;
ID ABB85862 standard; protein; 373 AA.
DE Murine adipocytes-derived protein.
PN W020016720-A1.
PD 13-SEP-2001.
PA (KITA/) KITAMURA T.
PA (TSUR/) TSURUGA H.
Query Match 8.7%; Score 146.5; DB 4; Length 373;
Best Local Similarity 25.9%; Pred. No. 0.00077;
ID AAB48126 standard; protein; 373 AA.
DE Mouse A236 polypeptide.
PN W0200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.6%; Score 145.5; DB 4; Length 373;
Best Local Similarity 25.9%; Pred. No. 0.00094;
ID AAB26449 standard; protein; 373 AA.
DE Mouse A236 protein.
PN US2002055139-A1.
PD 09-MAY-2002.
PA (HOLT/) HOLTZMAN D A.
PA (SHAR/) SHARP J D.
PA (LEIB/) LEIBY K R.
PA (BOSS/) BOSSONE S.
PA (PANT/) PANT Y.
PA (BARN/) BARNES T M.
PA (FRAS/) FRASER C C.
PA (WRIK/) WRIGHTON N.
PA (MYER/) MYERS P S.
PA (KING/) KINGSBURY G.
Query Match 8.6%; Score 145.5; DB 5; Length 373;
Best Local Similarity 25.9%; Pred. No. 0.00094;
ID ABB66424 standard; protein; 2016 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 26064.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 8.6%; Score 145; DB 4; Length 2016;
Best Local Similarity 25.6%; Pred. No. 0.01;
RESULT 1151

ID AAB48149 standard; protein; 373 AA.
DE Mouse A236 variant 2 polypeptide.
PN W0200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.6%; Score 144.5; DB 4; Length 373;
Best Local Similarity 26.1%; Pred. No. 0.0011;
ID AAB48150 standard; protein; 373 AA.
DE Mouse A236 variant 3 polypeptide.
PN W0200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.6%; Score 144.5; DB 4; Length 373;
Best Local Similarity 25.6%; Pred. No. 0.0011;
ID AAB48148 standard; protein; 373 AA.
DE Mouse A236 variant 1 polypeptide.
PN W0200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.6%; Score 144.5; DB 4; Length 373;
Best Local Similarity 26.1%; Pred. No. 0.0011;
ID ABB63044 standard; protein; 467 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15924.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 8.5%; Score 143.5; DB 4; Length 467;
Best Local Similarity 22.1%; Pred. No. 0.0019;
ID ABB63044 standard; protein; 396 AA.
DE Murine necln-like protein 1.
PN W02003064992-A2.
PD 07-AUG-2003.
PA (PLAN-) PLANET BIOTECHNOLOGY INC.
PA (LARR/) LARRICK J W.
PA (WYCO/) WYCOFF K L.
Query Match 8.4%; Score 142.5; DB 7; Length 396;
Best Local Similarity 19.6%; Pred. No. 0.0018;
ID ABB69287 standard; protein; 398 AA.
DE Amino acid sequence of long extracellular form of murine B7-1 (CD80).
PN W020008057-A2.
PD 17-FEB-2000.
PA (IMMV ) IMMUNEX CORP.
Query Match 8.4%; Score 142.5; DB 3; Length 398;
Best Local Similarity 19.6%; Pred. No. 0.0019;
ID AAE00868 standard; protein; 404 AA.
DE Mouse brain immunoglobulin superfamily receptor (Bigr) protein.
PN W0200129083-A1.
PD 26-APR-2001.
PA (TEKA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 8.4%; Score 142.5; DB 4; Length 404;
Best Local Similarity 19.6%; Pred. No. 0.0019;
ID ABB68257 standard; protein; 1395 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31563.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 8.4%; Score 142.5; DB 4; Length 1395;
Best Local Similarity 21.1%; Pred. No. 0.01;
```

RESULT 1160
ID ADE08000 standard; protein; 376 AA.
DE Novel protein (useful for identifying genetic disorders) #155.
PN W02003054152-A2.
PD 03-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 8.4%; Score 141.5; DB 7; Length 376;
Best Local Similarity 25.4%; Pred. No. 0.0021;
RESULT 1161
ID AAY13563 standard; protein; 1395 AA.
DE Drosophila Robo 1 polypeptide.
PN W0925833-A1.
PD 27-MAY-1999.
PA (REGC-) UNIV CALIFORNIA.
Query Match 8.4%; Score 141.5; DB 2; Length 1395;
Best Local Similarity 21.3%; Pred. No. 0.012;
RESULT 1162
ID AAY08401 standard; protein; 1395 AA.
DE Drosophila sp. Robo1 protein.
PN W0920764-A1.
PD 29-APR-1999.
PA (REGC-) UNIV CALIFORNIA.
Query Match 8.4%; Score 141.5; DB 2; Length 1395;
Best Local Similarity 21.3%; Pred. No. 0.012;
RESULT 1163
ID ADB85335 standard; protein; 1395 AA.
DE Fruitfly nerve cell growth modulator SLIT-1-associated sequence #1.
PN US2003170727-A1.
PD 11-SEP-2003.
PA (GOOD/) GOODMAN C S.
PA (KIDD/) KIDD T.
PA (BROS/) BROSE K.
PA (TESS/) TESSIER-LAVIGNE M.
Query Match 8.4%; Score 141.5; DB 7; Length 1395;
Best Local Similarity 21.3%; Pred. No. 0.012;
RESULT 1164
ID AAB71502 standard; protein; 1052 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41298.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 8.4%; Score 141; DB 4; Length 1052;
Best Local Similarity 25.1%; Pred. No. 0.0093;
RESULT 1165
ID AAM69698 standard; protein; 352 AA.
DE Mouse coxsackievirus and Ad2 and Ad5 receptor MCR protein.
PN W09383819-A1.
PD 06-AUG-1998.
PA (UYNY-) UNIV NEW YORK STATE.
Query Match 8.3%; Score 140.5; DB 2; Length 352;
Best Local Similarity 25.4%; Pred. No. 0.0023;
RESULT 1166
ID AAM57213 standard; protein; 376 AA.
DE Mouse coxsackievirus and adenovirus receptor.
PN W09811221-A2.
PD 19-MAR-1998.
PA (DAND-) DANA PARBER CANCER INST INC.
Query Match 8.3%; Score 140.5; DB 2; Length 376;
Best Local Similarity 25.4%; Pred. No. 0.0025;
RESULT 1167
ID ADP56685 standard; protein; 265 AA.
DE Human junction adhesion molecule 3 splice variant 2 (hujAM3sv2) protein.
PN W02004053058-A2.
PD 24-JUN-2004.
PA (ELIL-) LILLY & CO ELI.
Query Match 8.3%; Score 139.5; DB 8; Length 265;
Best Local Similarity 24.0%; Pred. No. 0.0019;
RESULT 1168
ID AAY96294 standard; protein; 310 AA.
DE Human IGFAM-6 immunoglobulin.
PN W0200029583-A2.
PD 25-MAY-2000.
PA (INCY-) INCYTE PHARM INC.

Query Match 8.3%; Score 139.5; DB 3; Length 310;
Best Local Similarity 22.0%; Pred. No. 0.0024;
RESULT 1169
ID ADP56683 standard; protein; 310 AA.
DE Human junction adhesion molecule 3 (hujAM3) full-length protein.
PN W02004053058-A2.
PD 24-JUN-2004.
PA (ELIL-) LILLY & CO ELI.
Query Match 8.3%; Score 139.5; DB 8; Length 310;
Best Local Similarity 22.0%; Pred. No. 0.0024;
RESULT 1170
ID AAY96735 standard; protein; 310 AA.
DE PRO1868, an A33 antigen homologue.
PN W0200036102-A2.
PD 22-JUN-2000.
PA (GETH-) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 3; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1171
ID AAB33457 standard; protein; 310 AA.
DE Human PRO1868 protein UNQ859 SEQ ID NO:193.
PN W0200053758-A2.
PD 14-SEP-2000.
PA (GETH-) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 3; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1172
ID AAB27276 standard; protein; 310 AA.
DE Human confuency regulated adhesion molecule 1 #2.
PN W0200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMP DICTAGENE SA.
Query Match 8.2%; Score 138.5; DB 3; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1173
ID AAB80272 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN W0200104311-A1.
PD 18-JAN-2001.
PA (GETH-) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1174
ID AAM93905 standard; protein; 310 AA.
DE Human polypeptide, SEQ ID NO: 4051.
PN RP1130094-A2.
PD 05-SEP-2001.
PA (HELT-) HELIX RES INST.
Query Match 8.2%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1175
ID AAM93323 standard; protein; 310 AA.
DE Human polypeptide, SEQ ID NO: 2845.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELT-) HELIX RES INST.
Query Match 8.2%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1176
ID AAU12440 standard; protein; 310 AA.
DE Human PRO1868 polypeptide sequence.
PN W0200140466-A2.
PD 07-JUN-2001.
PA (GETH-) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1177
ID AAB80383 standard; protein; 310 AA.
DE Secreted protein encoded by gene #13.
PN W0200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 4; Length 310;

Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1178
ID AAB80408 standard; protein; 310 AA.
DE Secreted protein encoded by gene #38.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1179
ID AAB80409 standard; protein; 310 AA.
DE Secreted protein encoded by gene #39.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1180
ID AAB92709 standard; protein; 310 AA.
DE Human secreted protein PRO1868.
PN US2002098506-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1181
ID AAB91361 standard; protein; 310 AA.
DE Novel human secreted protein #7.
PN US2002098505-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1182
ID AAB84947 standard; protein; 310 AA.
DE Human PRO1868 protein sequence SEQ ID NO:262.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1183
ID AAB65297 standard; protein; 310 AA.
DE Human albumin fusion protein #1972.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1184
ID AAB65296 standard; protein; 310 AA.
DE Human albumin fusion protein #1971.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1185
ID AAB65298 standard; protein; 310 AA.
DE Human albumin fusion protein #1973.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1186
ID AAB31401 standard; protein; 310 AA.
DE Human PRO1868 polypeptide.
PN US2002098507-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;

RESULT 1187
ID AAB95553 standard; protein; 310 AA.
DE Human angiotensin related protein PRO1868 SEQ ID NO: 262.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANU/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1188
ID AAB71650 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1189
ID AAB72377 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2002182618-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1190
ID AAB80867 standard; protein; 310 AA.
DE Human secreted and transmembrane polypeptide PRO1868.
PN US2002192668-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1191
ID AAB01784 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US200303156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1192
ID AAB71505 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1193
ID ADA57610 standard; protein; 310 AA.
DE Human secreted protein #592.
PN WO2002102894-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1194
ID ADA57611 standard; protein; 310 AA.

DE Human secreted protein #592.
PN W02002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1195
ID ADA57309 standard; protein; 310 AA.
DE Human secreted protein #592.
PN W02002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1196
ID ABP7127 standard; protein; 310 AA.
DE Human junctional adhesion molecule 3 (JAM3).
PN W02003006673-A2.
PD 23-JAN-2003.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1197
ID ABU81138 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1198
ID ABU71951 standard; protein; 310 AA.
DE Human secreted/transmembrane protein PRO1868.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1199
ID ABO01834 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1200
ID ABU6838 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1201
ID ABU54407 standard; protein; 310 AA.
DE Human secreted/transmembrane protein PRO1868.
PN US2002132240-A1.
PD 19-FEB-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1202
ID ABO47422 standard; protein; 310 AA.
DE Human secreted/transmembrane polypeptide PRO1868.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1203
ID ABG73314 standard; protein; 310 AA.
DE Human PRO1868 polypeptide.

PN US2002164646-A1.
PD 07-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1204
ID ABU59919 standard; protein; 310 AA.
DE Novel secreted and transmembrane protein PRO1868.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1205
ID ABO25109 standard; protein; 310 AA.
DE Human secreted/transmembrane protein (PRO) #269.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1206
ID ABU64559 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #63.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1207
ID ABU67405 standard; protein; 310 AA.
DE Human secreted protein PRO1868.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1208
ID ABO14925 standard; protein; 310 AA.
DE Human secreted / transmembrane polypeptide PRO1868.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1209
ID ABU60813 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #7.
PN US2002160392-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1210
ID ABU67114 standard; protein; 310 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 538.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1211
ID ABU81236 standard; protein; 310 AA.
DE Human PRO1917polypeptide.
PN US2003032060-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1212
ID ABU69682 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868-H30.
PN US2003017463-A1.

PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1213
ID ABO14864 standard; protein; 310 AA.
DE Human secreted / transmembrane polypeptide PRO1868.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1214
ID ADA46057 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003023238-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1215
ID ADA7648 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1216
ID ADB29627 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1217
ID ADA19138 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1218
ID ADA61761 standard; protein; 310 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1219
ID ADB19546 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1220
ID ADB28087 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1221
ID ADA86566 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082711-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1222
ID ADB16130 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1223
ID ADA47916 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1224
ID ADA18484 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1225
ID ABO32816 standard; protein; 310 AA.
DE Human secreted/transmembrane protein PRO1868.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1226
ID ADA67711 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1227
ID ADB30718 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1228
ID ADA86014 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1229
ID ADA97226 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1230
ID ADA79530 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1231
ID ADA87669 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1232
ID ADB16871 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1233
ID ABO34876 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1234
ID ADA16459 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1235
ID ADA91963 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1236
ID ADB15026 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1237
ID ADB18987 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1238
ID ADA94202 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1239
ID ADB20098 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
Query Match 8.2%; Score 138.5; DB 6; Length 310;

Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1240
ID ADB13410 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1241
ID ABO43417 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1242
ID ADA74664 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1243
ID ADA42604 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1244
ID ADB24897 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1245
ID ADA82421 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1246
ID ADA75384 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1247
ID ADA85462 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1248
ID ADA84910 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
Query Match 8.2%; Score 138.5; DB 6; Length 310;


```
RESULT 1249
ID ABO17554 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1250
ID ADB30166 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1251
ID ADA80694 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1252
ID ADA75936 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1253
ID ADA47161 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1254
ID ADB25457 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1255
ID ADA93633 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1256
ID ADB26983 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1257
ID ADB31270 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1258
ID ADB18435 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003054447-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1259
ID ADA61198 standard; protein; 310 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1260
ID ADB24345 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1261
ID ADA96674 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1262
ID ADA81246 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1263
ID ADA96122 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1264
ID ADB26431 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1265
ID ADB21916 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1266
ID ADA77695 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1267
ID ADB18435 standard; protein; 310 AA.
```

DE Human PRO polypeptide #269.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1268
ID ADA67118 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1269
ID ADA16883 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039669-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1270
ID ADA1312 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1271
ID ADA42180 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1272
ID ADA88221 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1273
ID ADA46609 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1274
ID ADA17527 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1275
ID ADA43030 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1276
ID ADB28639 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PA (GETH) GENENTECH INC.

PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1277
ID ADB29191 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1278
ID ABO01894 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003027256-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1279
ID ADA77143 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1280
ID ADA88773 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1281
ID ADA97778 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1282
ID ADB27535 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1283
ID ADB22468 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1284
ID ABO17615 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1285
ID ADA67159 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

```
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1286
ID ADB32020 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1287
ID ADB323793 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1288
ID ADB32515 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1289
ID ADB15578 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1290
ID ADB38830 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1291
ID ADB38278 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1292
ID ADB66750 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1293
ID ADB89630 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1294
ID ADB90562 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1295
ID ADB77948 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1296
ID ADB39663 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1297
ID ADB75084 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1298
ID ADB47286 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1299
ID ADB86893 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1300
ID ADB77498 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1301
ID ADB34655 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1302
ID ADB35759 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1303
ID ADB34103 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
```

RESULT 1304
ID ADB35207 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1305
ID ADB36311 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1306
ID ADB46706 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1307
ID ADC28731 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1308
ID ADC39931 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1309
ID ADC40445 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1310
ID ADC19269 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1311
ID ADC34569 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1312
ID ADC29624 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1313

ID ADC29155 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1314
ID ADC41040 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1315
ID ADC19697 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1316
ID ADC34145 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1317
ID ADC13215 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1318
ID AAE38826 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003077657-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1319
ID ADC50579 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1320
ID ADC72126 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1321
ID ADC60105 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1322
ID ADC53112 standard; protein; 310 AA.

DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1323
ID ADC57466 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1324
ID ADC60657 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1325
ID ADC51132 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1326
ID ADC65659 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1327
ID ADC54757 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1328
ID ADC53718 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1329
ID ADC59241 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1330
ID ADC56119 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1331
ID ADC58669 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.

PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1332
ID ADC12667 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1333
ID ADC74383 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1016.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1334
ID ADC74606 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1239.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1335
ID ADC74607 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1240.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1336
ID ADD03363 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1337
ID ADC90355 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1338
ID ADC69774 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1339
ID ADC48663 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1340
ID ADD10192 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194776-A1.

```
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1341
ID ADD04767 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1342
ID ADC80723 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1343
ID ADD11230 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1344
ID ADD10551 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN 05-JUN-2003.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1345
ID ADC48111 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1346
ID ADD05222 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1347
ID ADC80171 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1348
ID ADD11511 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1349
ID ADD09640 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1350
ID ADD04228 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1351
ID ADD03804 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1352
ID ADD41353 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1353
ID ADD52492 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1354
ID ADD53232 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1355
ID ADD53784 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1356
ID ADD37304 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1357
ID ADD51940 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1358
ID ADD02739 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
```

```
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1359
ID ADD38106 standard; protein; 310 AA.
DE Human secreted protein #289.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1360
ID ADD38009 standard; protein; 310 AA.
DE Human secreted protein #192.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1361
ID ADD38105 standard; protein; 310 AA.
DE Human secreted protein #288.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1362
ID ADD02173 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1363
ID ADD54355 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1364
ID ADD92672 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1365
ID ADD91568 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1366
ID ADB04182 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1367
ID ADB32479 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1368
ID ADB22411 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1369
ID ADD79635 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1370
ID ADB42171 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1371
ID ADB17988 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1372
ID ADD92120 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1373
ID ADB33583 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1374
ID ADB34135 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1375
ID ADB80187 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1376
ID ADD93224 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
```

RESULT 1377
ID ADE19644 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1378
ID ADE35056 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1379
ID ADE19092 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1380
ID ADE43288 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1381
ID ADD96077 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1382
ID ADE22963 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1383
ID ADD79081 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003201429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1384
ID ADE33031 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1385
ID ADE42723 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1386

ID ADD80739 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1387
ID ADD89767 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1388
ID ADE41051 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1389
ID ADE04850 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1390
ID ADE92979 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1391
ID ADE21688 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1392
ID ADG23329 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1393
ID ADF97664 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1394
ID ADG80728 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1395
ID ADG80176 standard; protein; 310 AA.

DE Human PRO polypeptide #269.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1396
ID ADH62558 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A. L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1397
ID ADH59539 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1398
ID ADH55468 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1399
ID ADH56020 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1400
ID ADI38318 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1401
ID ADI6439 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1402
ID ADI65188 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1403
ID ADI6387 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1404
ID ADH82201 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1405
ID ADH81549 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1406
ID ADI58518 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003170864-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1407
ID ADJ26586 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1408
ID ADM82718 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1409
ID ADNI6117 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1410
ID ADNI6746 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1411
ID ADNI5565 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1412
ID ADNI5013 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1413
ID ADE81275 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1668.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1414
ID ADE79501 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1415
ID ADE76723 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1416
ID ADE88087 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1417
ID ADE86491 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1418
ID ADE79925 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1419
ID ADE75939 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1420
ID ADE73601 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1421
ID ADE84512 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;

Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1422
ID ADE23515 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1423
ID ADE24067 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1424
ID ADE24710 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1425
ID ADE87535 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1426
ID ADE89401 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1427
ID ADE74136 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1428
ID ADE18540 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1429
ID ADE88849 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1430
ID ADE99690 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2% Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;

```
RESULT 1431
ID ADE94669 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1432
ID ADE91280 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1433
ID ADE95421 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1434
ID ADE93531 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1435
ID ADF35112 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1436
ID ADE98809 standard; protein; 310 AA.
DE Human secreted/cranmembrane protein, #65.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1437
ID ADE92427 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1438
ID ADE90728 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1439
ID ADE91875 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1440
ID ADE99236 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1441
ID ADG40706 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODD/) GODDARD P. J.
PA (GURN/) GURNEY A. L.
PA (MATH/) MATHER J. P.
PA (WILL/) WILLIAMS P. M.
PA (WOOD/) WOOD W. I.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1442
ID ADF74100 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1443
ID ADG02454 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1444
ID ADG22240 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1445
ID ADG20310 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1446
ID ADF98216 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1447
ID ADG24433 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 8; Length 310;
Pred. No. 0.0029;
RESULT 1448
ID ADF98787 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003208055-A1.
```

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1448
ID ADG03618 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1450
ID ADF99339 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1451
ID ADG16924 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1452
ID ADG05383 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1453
ID ADG19650 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1454
ID ADF73676 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1455
ID ADG13487 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1456
ID ADG08544 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1457
ID ADG15714 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1458
ID ADG03618 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1459
ID ADG06297 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1460
ID ADG23881 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1461
ID ADG04170 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1462
ID ADG25071 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1463
ID ADG07368 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1464
ID ADG07920 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1465
ID ADG55415 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1466
ID ADG61079 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1467
ID A0662183 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1468
ID A0692519 standard; protein; 310 AA.
DE Human secreted/cranemembrane protein, #65.
PN US2003207145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1469
ID A0682384 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1470
ID A0657623 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1471
ID A0657071 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1472
ID A0655967 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1473
ID A0658727 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1474
ID A0671093 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1475
ID A0692946 standard; protein; 310 AA.
DE Human secreted/cranemembrane protein, #65.
PN US2003207146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1485

Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1476
ID A0658175 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1477
ID A0653759 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1478
ID A0671645 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1479
ID A0681832 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1480
ID A0630794 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1481
ID A0612161 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1482
ID A0652583 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1483
ID A0654311 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1484
ID A0681280 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1485

```
ID ADG56519 standard; protein; 310 AA.  
DE Novel human secreted and transmembrane protein PRO1868.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1486  
ID ADH12785 standard; protein; 310 AA.  
DE Novel human secreted and transmembrane protein PRO1868.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1487  
ID ADG61631 standard; protein; 310 AA.  
DE Novel human secreted and transmembrane protein PRO1868.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1488  
ID ADH28718 standard; protein; 310 AA.  
DE Human PRO polypeptide #269.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1489  
ID ADG54863 standard; protein; 310 AA.  
DE Novel human secreted and transmembrane protein PRO1868.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1490  
ID ADG59903 standard; protein; 310 AA.  
DE Novel human secreted and transmembrane protein PRO1868.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1491  
ID ADH20735 standard; protein; 310 AA.  
DE Human secreted/transmembrane protein, #65.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1492  
ID ADH43695 standard; protein; 310 AA.  
DE Human PRO polypeptide #131.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1493  
ID ADH07590 standard; protein; 310 AA.  
DE Human secreted/transmembrane protein, #65.  
PN US2004006211-A1.  
PD 08-JAN-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOMSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1494  
ID ADH60135 standard; protein; 310 AA.  
DE Human secreted/transmembrane protein, #65.  
PN US2003215904-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1495  
ID ADH07163 standard; protein; 310 AA.  
DE Human secreted/transmembrane protein, #65.  
PN US2004005665-A1.  
PD 08-JAN-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOMSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1496  
ID ADH13327 standard; protein; 310 AA.  
DE Human PRO polypeptide #269.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1497  
ID ADH18905 standard; protein; 310 AA.  
DE Human secreted/transmembrane protein, #65.  
PN US2003152999-A1.  
PD 14-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1498  
ID ADI65625 standard; protein; 310 AA.  
DE Human secreted/transmembrane protein, #65.  
PN US2003148419-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1499  
ID ADI37884 standard; protein; 310 AA.  
DE Human secreted/transmembrane protein, #65.  
PN US2003096340-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;  
RESULT 1500  
ID ADG10070 standard; protein; 310 AA.  
DE Novel human secreted and transmembrane protein PRO1868.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 8.2%; Score 138.5; DB 8; Length 310;  
Best Local Similarity 21.8%; Pred. No. 0.0029;
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 06:06:41 ; Search time 116 Seconds

(without alignments)
1592.201 Million cell updates/sec

Title: US-10-767-374-2

Perfect score: 1688
Sequence: 1 MGILLGULLGLHGLTVDTYGR.....AYIMLCRKTSQGHVYEAAR 321Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 1500 summaries

Database :

1: uniprot_02:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1688	100.0	321	2 O6UX14	O6ux14 homo sapien
2	1688	100.0	321	2 AAQ88707	AAq88707 homo sapi
3	1688	100.0	399	2 Q9J279	Q9j279 homo sapien
4	728	43.1	280	2 O80WA3	O80wa3 mus musculu
5	178.5	10.6	299	1 JAM1_HUMAN	Jam1 human
6	178.5	10.6	299	2 AAC28379	Aac28379 homo sapi
7	178.5	10.6	299	2 BAC11436	Bac11436 homo sapi
8	178.5	10.6	299	2 AAC84556	Aac84556 homo sapi
9	178.5	10.6	319	1 A33_HUMAN	A33 human
10	177	10.5	319	2 AAH69705	Aah69705 homo sapi
11	177	10.5	319	2 AAH69723	Aah69723 homo sapi
12	177	10.5	319	2 AAH69745	Aah69745 homo sapi
13	177	10.5	319	2 AAH69761	Aah69761 homo sapi
14	177	10.5	319	2 AAH69789	Aah69789 homo sapi
15	172	10.2	7962	2 Q10465	Q10465 homo sapien
16	172	10.2	34350	2 O8W242	O8w242 homo sapien
17	169.5	10.0	298	1 JAM1_BOVIN	Jam1 bovin
18	169.5	10.0	365	2 O8WMT3	O8wmt3 bos taurus
19	169	10.0	300	2 Q8VC39	Q8vc39 mus musculu
20	168	10.0	300	1 JAM1_MOUSE	Jam1 mouse
21	167	9.9	300	1 Q9JHY1	Q9jhy1 rattus norv
22	167	9.9	300	2 AAH65309	Aah65309 rattus norv
23	167	9.9	319	2 Q9TUV9	Q9tuv9 sus scrofa
24	167	9.9	319	2 Q9TUV9	Q9tuv9 sus scrofa
25	166	9.8	319	1 A33_MOUSE	A33 mouse
26	159.5	9.4	344	2 Q9UKV4	Q9ukv4 mus musculu
27	158	9.4	365	1 CXAR_HUMAN	Cxar human
28	157.5	9.3	332	2 O6P359	O6p359 xenopus tro
29	157.5	9.3	332	2 AAH64174	Aah64174 xenopus t
30	156.5	9.3	5516	2 Q7Z248	Q7z248 brachydanto
31	156.5	9.3	5516	2 Q7Z248	Q7z248 brachydanto

32	156	9.2	289	2 Q7ZWT0	Q7zwt0 xenopus lae
33	156	9.2	335	2 Q9YGH1	Q9ygh1 gallus gall
34	156	9.2	335	2 Q9PWR4	Q9pwr4 gallus gall
35	153.5	9.1	373	2 Q9H6B4	Q9h6b4 homo sapien
36	153.5	9.1	373	2 AAQ88706	Aaq88706 homo sapi
37	153.5	9.1	512	2 Q96DN8	Q96dn8 homo sapien
38	153.5	9.1	5636	2 Q96RW7	Q96rw7 homo sapien
39	151	8.9	390	2 Q9H1X9	Q9h1x9 homo sapien
40	149.5	8.9	344	2 Q9R067	Q9r067 rattus norv
41	149.5	8.9	358	2 Q9R066	Q9r066 rattus norv
42	146.5	8.7	373	2 Q920S5	Q920s5 mus musculu
43	145.5	8.6	335	2 Q9YGV5	Q9ygv5 gallus gall
44	145.5	8.6	372	2 Q8KIG0	Q8kig0 rattus norv
45	145.5	8.6	372	2 Q8R373	Q8r373 mus musculu
46	145.5	8.6	1271	2 Q6U714	Q6u714 brachydanto
47	145.5	8.6	1271	2 AAQ85080	Aaq85080 brachydant
48	145	8.6	3950	2 Q7YRFS	Q7yrf5 canis fami
49	144.5	8.6	537	2 Q7PSJ8	Q7psj8 anopheles g
50	143.5	8.5	403	2 Q9VP08	Q9vp08 drosophila
51	143.5	8.5	1052	1 FGR2_DROME	Fgr2 drome
52	143	8.5	448	2 Q81GAS	Q81gas drosophila
53	142.5	8.4	372	2 Q90Y50	Q90y50 brachydanto
54	142.5	8.4	396	2 Q99N28	Q99n28 m neccin-11
55	142.5	8.4	1395	2 Q7KVK3	Q7kvk3 drosophila
56	142.5	8.4	1395	2 AAF6887	Aaf6887 drosophila
57	142.5	8.4	1429	2 Q9W213	Q9w213 drosophila
58	142.5	8.4	1429	2 AAM71113	Aam71113 drosophila
59	141.5	8.4	1395	2 Q44924	Q44924 drosophila
60	141	8.3	1052	2 Q9VUC8	Q9vuc8 drosophila
61	140.5	8.3	352	2 Q91W66	Q91w66 mus musculu
62	140.5	8.3	365	2 CXAR_MOUSE	Cxar mouse
63	140.5	8.3	365	2 Q9DBF8	Q9dbf8 mus musculu
64	140.5	8.3	397	2 Q6XRC3	Q6xrc3 homo sapien
65	140.5	8.3	397	2 AAP47270	Aap47270 homo sapi
66	140.5	8.3	4071	2 Q6KX21	Q6kx21 gallus gall
67	140.5	8.3	4071	2 CAES1322	Caes1322 gallus ga
68	140	8.3	1662	2 Q7QIV4	Q7qiv4 anopheles g
69	139.5	8.3	3410	2 Q7TND0	Q7tnd0 rattus norv
70	139.5	8.3	3707	1 FGBM_MOUSE	Fgbm mouse
71	139	8.2	377	2 Q9VQY0	Q9vqy0 drosophila
72	138.5	8.2	310	2 Q9BX67	Q9bx67 homo sapien
73	138.5	8.2	310	2 AAQ88701	Aaq88701 homo sapi
74	138.5	8.2	310	2 AAH12147	Aah12147 homo sapi
75	138.5	8.2	355	2 Q8WML8	Q8wml8 homo sapien
76	138.5	8.2	413	2 Q6ZNT1	Q6znt1 homo sapien
77	138.5	8.2	413	2 BAD18394	Bad18394 gallus gall
78	138.5	8.2	1323	2 Q08476	Q08476 gallus gall
79	138.5	8.2	4162	2 Q98918	Q98918 gallus gall
80	138	8.2	298	2 Q804R4	Q804r4 brachydanto
81	138	8.2	310	2 Q9DB87	Q9db87 mus musculu
82	138	8.2	360	1 HPL3_HUMAN	Hpl3 human
83	138	8.2	423	2 Q8BU57	Q8bu57 mus musculu
84	138	8.2	523	2 Q80Z82	Q80z82 mus musculu
85	138	8.2	569	1 SILF_MOUSE	Silf mouse
86	137.5	8.1	309	2 Q96FT1	Q96ft1 homo sapien
87	137.5	8.1	749	2 Q967D9	Q967d9 drosophila
88	137.5	8.1	902	2 Q81Q17	Q81q17 drosophila
89	137.5	8.1	903	2 Q9VOY1	Q9voy1 drosophila
90	137.5	8.1	903	2 Q967D8	Q967d8 drosophila
91	137.5	8.1	1508	2 Q6NR34	Q6nr34 drosophila
92	137.5	8.1	1508	2 Q9VOY2	Q9voy2 drosophila
93	137.5	8.1	1508	2 AAQ23565	Aaq23565 drosophila
94	137.5	8.1	1508	2 AAF51029	Aaf51029 drosophila
95	137.5	8.1	1531	2 Q967D7	Q967d7 drosophila
96	137.5	8.1	2022	2 Q7KQ05	Q7kq05 drosophila
97	137.5	8.1	2022	2 AAS64901	Aas64901 drosophila
98	137	8.1	310	2 Q9DLM9	Q9dlm9 mus musculu
99	137	8.1	310	2 Q9BEX4	Q9bex4 m junctiona
100	137	8.1	359	1 LACH_DROME	Lach drome
101	137	8.1	359	2 Q9V6C2	Q9v6c2 drosophila
102	137	8.1	1316	2 Q70B16	Q70b16 anopheles g
103	137	8.1	2016	2 Q8MKW6	Q8mkw6 drosophila
104	137	8.1	2016	2 Q8MKW7	Q8mkw7 drosophila

105	137	8.1	2016	2	Q9NBA1	Q9nba1 drosophila	178	129.5	7.7	1479	2	AAFS9040	AAFS9040 drosophila
106	137	8.1	2019	2	Q8MK08	Q8mk08 drosophila	179	129.5	7.7	1482	2	Q9V4Y0	Q9v4y0 drosophila
107	137	8.1	2828	2	Q9NR99	Q9nr99 homo sapien	180	129.5	7.7	1375	1	UN52 CABEL	Q06561 caenorhabdi
108	136.5	8.1	230	2	P97269	P97269 cavia porce	181	129	7.6	308	2	Q80WN3	Q80wn3 mus musculu
109	136	8.1	283	2	Q9V776	Q9vc76 drosophila	182	129	7.6	324	2	Q7TWM2	Q7twm2 mus musculu
110	136	8.1	584	2	Q9Y3Y8	Q9y3y8 homo sapien	183	129	7.6	343	2	Q8R4Y0	Q8r4y0 mus musculu
111	136	8.1	1827	2	Q9VSG5	Q9vsg5 drosophila	184	129	7.6	433	2	Q9V644	Q9v644 drosophila
112	136	8.1	1827	2	AAFS0456	AAFS0456 drosophila	185	129	7.6	1427	2	Q91562	Q91562 xenopus lae
113	135.5	8.0	298	2	Q8CSK9	Q8csk9 mus musculu	186	128.5	7.6	1040	2	Q6NZJ4	Q6nzj4 mus musculu
114	135	8.0	394	2	Q925F2	Q925f2 mus musculu	187	1040	7.6	1040	2	AAH6106	AAH6106 mus muscu
115	135	8.0	838	2	Q90YH1	Q90yh1 brachydanio	188	128.5	7.6	2053	2	Q81ZY4	Q81zy4 homo sapien
116	135	8.0	2013	2	Q9ERC8	Q9erc8 mus musculu	189	128	7.6	255	2	Q9V064	Q9v064 drosophila
117	135	8.0	2013	2	Q8VH28	Q8vh28 rattus norv	190	128	7.6	257	2	Q8R202	Q8r202 mus musculu
118	134.5	8.0	303	2	Q8CE95	Q8ce95 mus musculu	191	128	7.6	261	2	Q9D7L8	Q9d7l8 mus muscu
119	134.5	8.0	303	2	Q7ZXR4	Q7zxr4 xenopus lae	192	128	7.6	261	2	AAH61082	AAH61082 mus muscu
120	134.5	8.0	450	2	Q6UX10	Q6ux10 homo sapien	193	128	7.6	343	2	Q8BY54	Q8by54 mus musculu
121	134.5	8.0	450	2	AAQ88711	AAq88711 homo sapi	194	128	7.6	344	2	Q9VYJ3	Q9vyj3 drosophila
122	134.5	8.0	2597	2	Q6WRH9	Q6wrh9 rattus norv	195	128	7.6	386	2	Q8B1N0	Q8b1n0 mus musculu
123	134.5	8.0	2597	2	AAQ16157	AAq16157 rattus no	196	128	7.6	392	2	Q7PSN2	Q7psn2 anopheles g
124	134	7.9	2217	2	Q8AV57	Q8av57 gallus gall	197	128	7.6	417	2	BAC29767	Bac29767 m 6 days
125	134	7.9	2623	2	Q6WR10	Q6wr10 homo sapien	198	128	7.6	977	2	Q96RD9	Q96rd9 homo sapien
126	134	7.9	2623	2	AAO16156	AAq16156 homo sapi	199	127.5	7.6	299	2	Q7Q8F3	Q7q8f3 anopheles g
127	133.5	7.9	321	2	Q61NFO	Q61nf0 xenopus lae	200	127.5	7.6	1028	2	Q61NBS	Q61nbs xenopus lae
128	133.5	7.9	321	2	AAH72333	AAh72333 xenopus 1	201	127.5	7.6	1028	2	AAH72368	AAh72368 xenopus 1
129	133.5	7.9	338	2	Q8N126	Q8n126 homo sapien	202	127.5	7.6	1340	2	Q8ND42	Q8nd42 homo sapien
130	133.5	7.9	338	2	AAQ88698	AAq88698 homo sapi	203	127.5	7.6	1906	1	XM5S CHICK	P11799 gallus gall
131	133.5	7.9	432	2	Q9UUP1	Q9uup1 homo sapien	204	127.5	7.6	1906	1	AAFC35031	AAfc35031 gallus ga
132	133.5	7.9	434	2	Q6DN72	Q6dn72 homo sapien	205	127	7.5	285	2	Q8BTK0	Q8btk0 mus musculu
133	133.5	7.9	484	2	Q26475	Q26475 schistocerc	206	127	7.5	337	1	OPCM CHICK	Q98892 gallus gall
134	133.5	7.9	487	2	Q7T2H2	Q7t2h2 gallus gall	207	127	7.5	337	1	Q9DF61	Q9df61 gallus gall
135	133.5	7.9	5175	2	Q810L3	Q810l3 caenorhabdi	208	127	7.5	632	2	Q6ZRX5	Q6zrx5 homo sapien
136	133.5	7.9	5198	2	Q76518	Q76518 caenorhabdi	209	127	7.5	632	2	BAC87305	Bac87305 homo sapi
137	133	7.9	305	2	Q8VIM2	Q8vim2 mus musculu	210	127	7.5	1459	2	Q90Z04	Q90z04 xenopus lae
138	133	7.9	349	1	LACH SCHAM	Q26474 schistocerc	211	127	7.5	1544	2	Q7P8H8	Q7p8h8 anopheles g
139	133	7.9	344	2	Q7ZXK1	Q7zxx1 xenopus lae	212	127	7.5	2053	2	Q8XKU7	Q8xku7 homo sapien
140	133	7.9	463	2	BAC28450	Bac28450 m adult p	213	127	7.5	2092	2	Q76MU9	Q76mu9 homo sapien
141	133	7.9	463	2	BAC34294	Bac34294 m adult p	214	127	7.5	2092	2	BAAB6446	Baa66446 homo sapi
142	133	7.9	697	2	Q8NC72	Q8nc72 homo sapien	215	127	7.5	2133	2	Q8RTD84	Q8rtd84 homo sapien
143	133	7.9	1059	2	Q6UXL7	Q6uxl7 homo sapien	216	127	7.5	2133	2	Q7POG9	Q7pog9 anopheles g
144	133	7.9	1059	2	AAQ88662	AAq88662 homo sapi	217	126.5	7.5	442	2	Q6NM88	Q6nm88 brachydanio
145	133	7.9	1106	1	PGDR_HUMAN	P09619 homo sapien	218	126.5	7.5	442	2	AAH67661	AAh67661 brachydan
146	133	7.9	1119	1	Q6UXM1	Q6uxm1 homo sapien	219	126.5	7.5	812	2	Q8N612	Q8n612 homo sapien
147	133	7.9	1119	2	AAQ88655	AAq88655 homo sapi	220	126.5	7.5	924	1	IC4S_HUMAN	Q9unf0 homo sapien
148	132.5	7.8	298	2	Q9J159	Q9j159 m vascular	221	126.5	7.5	924	2	Q8TAM9	Q8tam9 homo sapien
149	132.5	7.8	298	2	AAH28778	AAh28778 mus muscu	222	126.5	7.5	1056	2	Q90Z03	Q90z03 xenopus lae
150	132.5	7.8	765	2	Q9TWA4	Q9twa4 aplysia cal	223	126	7.5	318	2	Q91664	Q91664 xenopus lae
151	132.5	7.8	765	2	Q9BKQ1	Q9bkq1 aplysia cal	224	126	7.5	413	2	Q7QBV2	Q7qbv2 anopheles g
152	132.5	7.8	812	2	Q9TWAS	Q9twas aplysia cal	225	126	7.5	539	2	BAC28314	Bac28314 m adult m
153	132.5	7.8	812	2	Q9BKQ0	Q9bkq0 aplysia cal	226	126	7.5	885	2	Q8HYV1	Q8hyv1 sus scrofa
154	132.5	7.8	932	2	Q9TWA6	Q9twa6 aplysia cal	227	126	7.5	885	2	Q8HYV2	Q8hyv2 sus scrofa
155	132.5	7.8	932	2	Q9BKP9	Q9bkp9 aplysia cal	228	126	7.5	948	2	Q9VME2	Q9vme2 drosophila
156	132.5	7.8	1369	1	NFAS_CHICK	Q42414 gallus gall	229	126	7.5	948	2	AAFS2377	AAfs2377 drosophila
157	132	7.8	300	2	Q7SYQ7	Q7syq7 xenopus lae	230	126	7.5	1235	2	Q7Q0S7	Q7q0s7 anopheles g
158	132	7.8	1746	2	Q8WY19	Q8wy19 homo sapien	231	126	7.5	1431	2	Q8U060	Q8u060 mus musculu
159	132	7.8	2012	1	DSCA_HUMAN	Q60469 homo sapien	232	125.5	7.4	303	2	Q7Q154	Q7q154 anopheles g
160	131.5	7.8	461	2	Q13854	Q13854 homo sapien	233	125.5	7.4	412	2	Q9R1B1	Q9r1b1 rattus norv
161	131.5	7.8	1117	2	Q6PIC6	Q6pic6 mus musculu	234	125.5	7.4	707	2	Q7PMU1	Q7pmu1 anopheles g
162	131.5	7.8	1117	2	AAH65142	AAh65142 mus muscu	235	125.5	7.4	1443	2	Q8WTR2	Q8wtr2 drosophila
163	131.5	7.8	2673	2	Q96SC3	Q96sc3 homo sapien	236	125.5	7.4	1496	2	Q92626	Q92626 homo sapien
164	131	7.8	259	2	Q9Y582	Q9y582 homo sapien	237	125.5	7.4	1765	2	Q9V830	Q9v830 drosophila
165	131	7.8	285	2	Q9D780	Q9d780 mus musculu	238	125.5	7.4	1770	2	Q9V829	Q9v829 drosophila
166	131	7.8	714	2	Q6ZPE6	Q6zpe6 mus musculu	239	125	7.4	313	2	Q5Y596	Q5y596 gallus gall
167	131	7.8	714	2	BAC98291	Bac98291 mus muscu	240	125	7.4	315	2	Q9DGI5	Q9dgi5 gallus gall
168	131	7.8	4391	1	PGBM_HUMAN	P98160 homo sapien	241	125	7.4	1006	2	Q6IDB9	Q6idb9 drosophila
169	130.5	7.7	272	2	Q70J56	Q70j56 mus musculu	242	125	7.4	1006	2	AAH72780	AAh72780 drosophila
170	130	7.7	253	2	Q9DBH2	Q9dbh2 m mus muscu	243	124.5	7.4	259	2	Q7Z2Q1	Q7z2q1 homo sapien
171	130	7.7	285	2	Q8VE93	Q8ve93 mus musculu	244	124.5	7.4	344	2	Q93242	Q93242 gallus gall
172	130	7.7	515	1	PVRI_PIG	Q9g176 sus scrofa	245	124.5	7.4	353	1	CEPU_CHICK	Q90732 gallus gall
173	130	7.7	582	2	Q8R4B5	Q8r4b5 mus musculu	246	124.5	7.4	387	2	Q86XK7	Q86xk7 homo sapien
174	130	7.7	915	2	Q8R4B3	Q8r4b3 mus musculu	247	124.5	7.4	412	2	Q6WZS4	Q6wzs4 homo sapien
175	130	7.7	955	1	MDG1_HUMAN	Q8nfP4 homo sapien	248	124.5	7.4	412	2	CAE45954	Caef5954 homo sapi
176	129.5	7.7	1040	1	AXOI_RAT	P22063 rattus norv	249	124.5	7.4	877	2	Q9GSH3	Q9gsh3 halocynthia
177	129.5	7.7	1479	2	Q7KQTS	Q7kqts drosophila	250	124.5	7.4	1073	2	Q9W1T8	Q9wit8 drosophila

251	124.5	7.4	1173	2	06NR54	06nr54 drosophila	324	121.5	7.2	1299	2	AA89825	AA89825 ractus no
252	124.5	7.4	1173	2	AAQ23543	AAQ23543 homo sapien	325	121.5	7.2	1842	2	081ZY3	081zy3 homo sapien
253	124	7.3	311	2	06DN73	06dn73 xenopus lae	326	121	7.2	366	2	06NVZ3	06nvz3 homo sapi
254	124	7.3	394	2	06DCT6	06dct6 pan troglod	327	121	7.2	366	2	AAH67808	AAH67808 homo sapi
255	124	7.3	597	1	SIL, PANTR	095110 pan troglod	328	121	7.2	410	2	07YZA7	07yza7 bombyx mori
256	124	7.3	623	2	08BY18	08by18 mus musculu	329	121	7.2	467	2	091VT9	091vt9 mus musculu
257	124	7.3	688	2	080ZB3	080z3 mus musculu	330	121	7.2	528	2	P91670	P91670 drosophila
258	124	7.3	697	2	07PMJ7	07pmj7 anopheles g	331	121	7.2	532	2	06NMU3	06nmu3 drosophila
259	124	7.3	853	1	NCAL_BOVIN	P18136 bos taurus	332	121	7.2	532	2	09YUFO	09yuf0 drosophila
260	124	7.3	1240	1	NPAS_HUMAN	094856 homo sapien	333	121	7.2	532	2	AAH88551	AAH88551 drosophila
261	124	7.3	1240	1	NPAS_MOUSE	081003 mus musculu	334	121	7.2	858	2	018466	018466 hirtudo medi
262	124	7.3	1240	1	NPAS_RAT	P97685 ractus norv	335	121	7.2	1031	2	090YME	090yme brachydanio
263	124	7.3	1251	2	06Z054	06z054 mus musculu	336	121	7.2	1086	2	07OH02	07oh02 anopheles g
264	124	7.3	1251	2	BAC98017	Bac98017 mus muscu	337	121	7.2	1155	2	07Q3X8	07q3x8 anopheles g
265	124	7.3	1366	1	ROB3_MOUSE	Q92214 mus musculu	338	121	7.2	1304	1	NRCA_HUMAN	092823 homo sapien
266	124	7.3	1730	2	07YRQ7	Q7YRQ7 sus scrofa	339	120.5	7.1	163	3	08K1H8	08k1h8 mus musculu
267	123.5	7.3	316	2	07TPB4	Q7TPB4 ractus norv	340	120.5	7.1	202	2	06NVA1	06nva1 homo sapien
268	123.5	7.3	338	1	LAMP_CHICK	098919 gallus gall	341	120.5	7.1	202	2	AAH69185	AAH69185 homo sapi
269	123.5	7.3	350	2	002869	002869 gallus gall	342	120.5	7.1	265	2	07PUY3	07puv3 anopheles g
270	123.5	7.3	383	2	075MW9	Q75m19 homo sapien	343	120.5	7.1	358	2	09Q490	09q490 brachydanio
271	123.5	7.3	383	2	AA507434	AA507434 homo sapi	344	120.5	7.1	440	2	AAQ88700	AAQ88700 homo sapi
272	123.5	7.3	412	2	063611	Q63611 ractus norv	345	120.5	7.1	442	1	SIL, HUMAN	043659 homo sapien
273	123.5	7.3	454	2	091WE4	Q91WE4 mus musculu	346	120.5	7.1	442	2	09BY67	09by67 homo sapien
274	123.5	7.3	521	1	CEAL_MOUSE	P31809 mus musculu	347	120.5	7.1	442	2	CAG33438	Cag33438 homo sapi
275	123.5	7.3	521	2	0925F3	0925f3 mus musculu	348	120.5	7.1	482	2	BAC26124	Bac26124 mus muscu
276	123.5	7.3	605	2	0921P2	0921p2 mus musculu	349	120.5	7.1	529	2	091V87	091v87 mus musculu
277	123.5	7.3	815	2	0805B9	0805b9 brachydanio	350	120.5	7.1	529	2	AAH58745	AAH58745 mus muscu
278	123.5	7.3	838	2	08BQ96	08bq96 mus musculu	351	120.5	7.1	538	2	Q28939	Q28939 sus scrofa
279	123.5	7.3	838	2	08C4B2	08c4b2 mus musculu	352	120.5	7.1	549	2	09JUB9	09jub9 mus musculu
280	123.5	7.3	1091	1	NCAL_CHICK	P13590 gallus gall	353	120.5	7.1	1940	2	06PDN3	06pdn3 mus musculu
281	123.5	7.3	1151	2	09OVN5	09ovn5 ractus ap.	354	120.5	7.1	1940	2	AAH58610	AAH58610 mus muscu
282	123.5	7.3	1256	1	NRCA_MOUSE	Q81004 mus musculu	355	120	7.1	304	2	09BPN5	09bpn5 caenorhabdi
283	123	7.3	265	2	Q9NGZ0	Q9ngz0 epodoptera	356	120	7.1	312	2	06UXG6	06uxg6 homo sapien
284	123	7.3	344	1	NTRI_HUMAN	Q9P121 homo sapien	357	120	7.1	312	2	AAQ88727	AAQ88727 homo sapi
285	123	7.3	344	2	AAQ88697	AAQ88697 homo sapi	358	120	7.1	410	2	06R3L9	06r3l9 bombyx mand
286	123	7.3	439	2	057349	057349 gallus gall	359	120	7.1	410	2	AA500446	AA500446 bombyx ma
287	123	7.3	464	2	06GL25	06gl25 xenopus tro	360	120	7.1	641	2	086SD2	086sd2 clona lntes
288	123	7.3	538	2	Q29123	Q29123 sus scrofa	361	120	7.1	1033	2	Q24327	Q24327 drosophila
289	123	7.3	1247	2	Q7Q0S6	Q7q0s6 anopheles g	362	120	7.1	1033	2	Q9V643	Q9v643 drosophila
290	122.5	7.3	400	2	08HY16	08hy16 cebus apelli	363	120	7.1	1036	1	AXOI_CHICK	P28655 gallus gall
291	122.5	7.3	761	1	NCAL_HUMAN	P13591 homo sapien	364	120	7.1	1093	3	096VJ1	096vj1 homo sapien
292	122.5	7.3	848	1	NCAL_HUMAN	Q8uv66 brachydanio	365	120	7.1	1094	2	09BYB8	09byb8 homo sapien
293	122.5	7.3	1032	2	08UVJ6	08uvj6 brachydanio	366	119.5	7.1	298	1	JAM2_HUMAN	06yvc1 homo sapien
294	122.5	7.3	1073	2	094898	094898 homo sapien	367	119.5	7.1	298	2	06VNC1	AA182538 homo sapi
295	122.5	7.3	1284	1	NRCA_CHICK	P93331 gallus gall	368	119.5	7.1	298	2	AAH2538	AAH2538 homo sapi
296	122.5	7.3	1419	2	0985W3	Q985w3 brachydanio	369	119.5	7.1	307	2	BAC35705	Bac35705 m 2 days
297	122.5	7.3	18412	2	Q7Z261	Q7z261 brachydanio	370	119.5	7.1	373	2	Q7KXP5	Q7kxp5 homo sapien
298	122	7.2	240	2	06MG96	06mg96 ractus norv	371	119.5	7.1	463	1	SIL, HUMAN	09y316 homo sapien
299	122	7.2	240	2	CAE83950	CAE83950 ractus no	372	119.5	7.1	463	2	Q16170	Q16170 homo sapien
300	122	7.2	410	2	06R3M2	Q6r3m2 bombyx mori	373	119.5	7.1	468	2	096CA7	096ca7 homo sapien
301	122	7.2	410	2	AA500443	AA500443 bombyx mo	374	119.5	7.1	463	2	Q9UFI4	Q9ufi4 homo sapien
302	122	7.2	433	2	06DJ83	Q6dj83 xenopus tro	375	119.5	7.1	526	1	CEAL_HUMAN	P13668 homo sapien
303	122	7.2	1166	2	09OVN4	Q9ovn4 ractus ap.	376	119.5	7.1	529	2	Q7TOM3	Q7tom3 ractus norv
304	121.5	7.2	320	2	07OOP8	Q7o0p8 anopheles g	377	119.5	7.1	549	2	Q9D006	Q9d006 mus musculu
305	121.5	7.2	344	1	CEA6_HUMAN	P40159 homo sapien	378	119.5	7.1	725	1	NCAL_MOUSE	P13594 mus musculu
306	121.5	7.2	344	2	AAH8776	AAH8776 homo sapi	379	119.5	7.1	725	2	Q73634	Q73634 xenopus lae
307	121.5	7.2	349	2	09NOS3	Q9ng87 homo sapien	380	119.5	7.1	734	2	Q9NQT2	Q9ngt2 homo sapien
308	121.5	7.2	595	2	06ZRB5	Q6zrb5 homo sapien	381	119.5	7.1	1115	1	NCAL_MOUSE	P13595 mus musculu
309	121.5	7.2	595	2	BAC87234	Bac87234 homo sapi	382	119.5	7.1	1643	2	Q7QCT8	Q7qct8 anopheles g
310	121.5	7.2	1154	2	09OVN3	Q9ovn3 ractus ap.	383	119.5	7.1	1950	2	080YH8	080yh8 mus musculu
311	121.5	7.2	1194	2	06PMJ5	Q6pmj5 ractus norv	384	119	7.0	334	2	002870	Q02870 gallus gall
312	121.5	7.2	1194	2	AA898824	AA898824 ractus no	385	119	7.0	337	2	P97268	P97268 cavia porce
313	121.5	7.2	1197	2	06PW38	Q6pw38 ractus norv	386	119	7.0	410	2	Q6R3M0	Q6r3m0 bombyx mori
314	121.5	7.2	1197	2	AA898821	AA898821 ractus no	387	119	7.0	410	2	AA500444	AA500444 bombyx mo
315	121.5	7.2	1198	2	06PMJ7	Q6pmj7 ractus norv	388	119	7.0	410	2	AA500445	AA500445 bombyx mo
316	121.5	7.2	1198	2	AA898822	AA898822 ractus no	389	119	7.0	467	2	08CGF2	08cgf2 mus musculu
317	121.5	7.2	1206	2	06PMJ6	Q6pmj6 ractus norv	390	119	7.0	727	2	06RKX2	Q6rkx2 ractus norv
318	121.5	7.2	1206	2	AA898823	AA898823 ractus no	391	119	7.0	727	2	AA518426	AA518426 ractus no
319	121.5	7.2	1209	2	06PMJ9	Q6pmj9 ractus norv	392	119	7.0	779	2	Q9Y136	Q9y136 manduca sex
320	121.5	7.2	1214	1	AA898820	AA898820 ractus no	393	119	7.0	837	2	Q9Y137	Q9y137 manduca sex
321	121.5	7.2	1224	2	NRCA_RAT	P97686 ractus norv	394	119	7.0	837	2	Q6RKX3	Q6rkx3 ractus norv
322	121.5	7.2	1224	2	000573	000573 homo sapien	395	119	7.0	837	2	AA518425	AA518425 ractus no
323	121.5	7.2	1299	2	06PMJ4	Q6pmj4 ractus norv	396	119	7.0	895	2	BAC34837	Bac34837 m 12 days

397	119	7.0	1091	2	P70193	P70193 mus musculus	470	117	6.9	448	2	O9JHL7	O9Jhl7 rattus norv
398	119	7.0	1994	2	O6ZP2	O6ZP2 mus musculus	471	117	6.9	459	2	O9JHL6	O9Jhl6 rattus norv
399	119	7.0	1994	2	BAC98189	BAC98189 mus muscu	472	117	6.9	595	1	SILL_HUMAN	O96q01 homo sapien
400	119	7.0	2176	2	O6V4S5	O6V4S5 mus musculus	473	117	6.9	739	1	VCA1_RAT	P13596 rattus norv
401	119	7.0	2176	2	AAQ57661	AAQ57661 mus muscu	474	117	6.9	858	1	NCA1_RAT	P13596 rattus norv
402	119	7.0	4463	2	O8MLD8	O8MLD8 drosophila	475	117	6.9	1062	2	O8BRK3	O8BRK3 mus musculus
403	119	7.0	9270	2	O8MLD9	O8MLD9 drosophila	476	117	6.9	1062	2	AAQ10071	AAQ10071 mus muscu
404	119	7.0	26926	2	O10466	O10466 homo sapien	477	117	6.9	1445	2	O6J155	O6J155 rattus norv
405	119	7.0	26926	2	O8WZB3	O8WZB3 homo sapien	478	117	6.9	1447	1	DCC_HUMAN	P43146 homo sapien
406	118.5	7.0	152	2	O8BSO8	O8BSO8 mus musculus	479	117	6.9	2164	1	O91AR9	O91AR9 gallus gall
407	118.5	7.0	282	2	O6UXZ0	O6UXZ0 homo sapien	480	116.5	6.9	285	2	O7PNT4	O7Pnt4 anopheles g
408	118.5	7.0	262	2	AAQ88520	AAQ88520 homo sapi	481	116.5	6.9	338	1	LAMP_RAT	O6Zk13 rattus norv
409	118.5	7.0	282	2	O7TPU2	O7TPU2 mus musculus	482	116.5	6.9	341	2	O8BLK3	O8BLK3 mus musculus
410	118.5	7.0	282	2	O8VIM1	O8VIM1 mus musculus	483	116.5	6.9	361	2	O6VUH9	O6Vuh9 rattus norv
411	118.5	7.0	333	1	AMAL_DHOME	P15364 drosophila	484	116.5	6.9	361	2	AAQ91613	AAQ91613 rattus no
412	118.5	7.0	341	2	O7KSX2	O7KSX2 drosophila	485	116.5	6.9	445	2	O8K3T6	O8K3T6 mus musculus
413	118.5	7.0	341	2	AAH13372	AAH13372 drosophil	486	116.5	6.9	554	2	O9W4R3	O9W4R3 drosophila
414	118.5	7.0	413	2	O7OBU1	O7qbu1 anopheles g	487	116.5	6.9	806	1	CEK2_CHICK	P18460 gallus gall
415	118.5	7.0	439	2	O6GTU4	O6gtu4 homo sapien	488	116.5	6.9	899	2	O7PQM9	O7Pqm9 anopheles g
416	118.5	7.0	458	2	O63093	O63093 rattus norv	489	116.5	6.9	972	2	O26614	O26614 strongyloce
417	118.5	7.0	457	1	SILL_HUMAN	O9Y286 homo sapien	490	116.5	6.9	1040	1	AXO1_HUMAN	O02246 homo sapien
418	118.5	7.0	510	2	O9ENV8	O9ENV8 homo sapien	491	116.5	6.9	1051	1	PTX7_CHICK	O91048 gallus gall
419	118.5	7.0	510	2	AAH10423	AAH10423 homo sapi	492	116.5	6.9	1598	2	O9P214	O9P214 homo sapien
420	118.5	7.0	519	1	ECTO_RAT	P16573 rattus norv	493	116	6.9	237	2	O6DOX5	O6dX5 oryctolagus
421	118.5	7.0	519	2	AAH61740	AAH61740 rattus no	494	116	6.9	344	1	NTRI_RAT	O6d218 rattus norv
422	118.5	7.0	542	2	BAC27034	BAC27034 m adult m	495	116	6.9	1027	2	O9OW79	O9OW79 gallus gall
423	118.5	7.0	947	1	MUSK_CHICK	O8AXY6 gallus gall	496	116	6.9	1103	2	O6ONF3	O6onf3 canis fami
424	118.5	7.0	1011	2	O24273	O24273 drosophila	497	116	6.9	1103	2	AA548371	AA548371 canis fam
425	118.5	7.0	1476	2	O7Q029	O7qj29 anopheles g	498	116	6.9	1447	1	DCC_MOUSE	P70211 mus musculus
426	118.5	7.0	1561	2	O924D2	O924D2 mus musculus	499	116	6.9	1709	1	SN_HUMAN	O9b222 homo sapien
427	118.5	7.0	1694	1	SN_MOUSE	O62230 mus musculus	500	116	6.9	6658	2	O76281	O76281 drosophila
428	118	7.0	344	1	NTRI_MOUSE	O99p10 mus musculus	501	116	6.9	8647	2	O7RK05	O7RKp5 drosophila
429	118	7.0	344	2	O8BG33	O8BG33 m mus muscu	502	116	6.9	8647	2	AA564601	AA564601 drosophi
430	118	7.0	359	2	O7ZX17	O7zx17 xenopus lae	503	116	6.9	8648	2	O7KOP6	O7Kdp6 drosophila
431	118	7.0	351	2	O7QJG1	O7qjg1 anopheles g	504	116	6.9	8648	2	AA564600	AA564600 drosophi
432	118	7.0	413	2	O9VAR6	O9var6 drosophila	505	116	6.9	8930	2	O7RK07	O7RKp7 drosophila
433	118	7.0	450	2	O9VAR25	O9var25 drosophila	506	116	6.9	8930	2	AA564599	AA564599 drosophi
434	118	7.0	501	2	O6O147	O6o147 bos taurus	507	116	6.9	8943	2	O9V4F7	O9V4F7 drosophila
435	118	7.0	501	2	AA573243	AA573243 bos tauri	508	115.5	6.8	295	2	O9Z2H8	O9Z2H8 mus musculus
436	118	7.0	540	2	O8NOZ9	O8NOZ9 homo sapien	509	115.5	6.8	295	2	O9OYL6	O9OYL6 mus musculus
437	118	7.0	547	1	ICA3_HUMAN	P12942 homo sapien	510	115.5	6.8	309	1	CD86_MOUSE	P42082 mus musculus
438	118	7.0	547	2	O6PD68	O6pd68 homo sapien	511	115.5	6.8	309	2	AAAD25880	AAAD25880 mus muscu
439	118	7.0	547	2	AAH58903	AAH58903 homo sapi	512	115.5	6.8	309	2	AAAD25881	AAAD25881 mus muscu
440	118	7.0	626	2	O6DCH3	O6dch3 xenopus lae	513	115.5	6.8	309	2	AAAD25882	AAAD25882 mus muscu
441	118	7.0	837	1	NCM2_MOUSE	O35136 mus musculus	514	115.5	6.8	309	2	AAAD25883	AAAD25883 mus muscu
442	118	7.0	1238	1	VGR1_HUMAN	P17948 h vasculat	515	115.5	6.8	309	2	BAC37666	BAC37666 mus muscu
443	118	7.0	4824	2	O95YH1	O95YH1 procambiarus	516	115.5	6.8	314	2	O61238	O61238 mus musculus
444	118	7.0	17352	2	O95YH2	O95YH2 procambiarus	517	115.5	6.8	356	2	O64381	O64381 mus musculus
445	117.5	7.0	309	2	O91YV7	O91YV7 mus musculus	518	115.5	6.8	390	2	O6P500	O6P500 rattus norv
446	117.5	7.0	316	2	O8VE98	O8VE98 mus musculus	519	115.5	6.8	390	2	AAH63181	AAH63181 rattus no
447	117.5	7.0	316	2	AAH56608	AAH56608 mus muscu	520	115.5	6.8	445	2	O8R4L1	O8R4L1 mus musculus
448	117.5	7.0	338	1	LAMP_HUMAN	O13449 homo sapien	521	115.5	6.8	520	2	O925P2	O925P2 mus musculus
449	117.5	7.0	338	2	O8IV49	O8IV49 homo sapien	522	115.5	6.8	725	2	O7J633	O7J633 xenopus lae
450	117.5	7.0	340	2	O9W3N2	O9W3N2 drosophila	523	115.5	6.8	734	2	O9NP65	O9NP65 homo sapien
451	117.5	7.0	344	2	O13774	O13774 homo sapien	524	115.5	6.8	734	2	O9NPB7	O9NPB7 homo sapien
452	117.5	7.0	437	2	AAH35359	AAH35359 homo sapi	525	115.5	6.8	734	2	O9NPQ9	O9NPQ9 homo sapien
453	117.5	7.0	509	2	O920C2	O920C2 mus musculus	526	115.5	6.8	734	2	O9NQO9	O9NQO9 homo sapien
454	117.5	7.0	775	2	O6PFS0	O6PFS0 xenopus lae	527	115.5	6.8	734	2	O9NQO7	O9NQO7 homo sapien
455	117.5	7.0	775	2	AAH57728	AAH57728 xenopus l	528	115.5	6.8	734	2	O9NQO1	O9NQO1 homo sapien
456	117.5	7.0	800	2	O918X3	O918X3 brachydantio	529	115.5	6.8	734	2	O96RF5	O96RF5 homo sapien
457	117.5	7.0	858	2	O86X47	O86X47 homo sapien	530	115.5	6.8	734	2	O96RF6	O96RF6 homo sapien
458	117.5	7.0	1028	2	P97528	P97528 rattus norv	531	115.5	6.8	738	1	PECL_HUMAN	P16284 homo sapien
459	117.5	7.0	1056	2	O7ZW34	O7ZW34 brachydantio	532	115.5	6.8	738	1	O8TRH1	O8TRH1 homo sapien
460	117.5	7.0	1092	1	NCA2_XENTLA	P36335 xenopus lae	533	115.5	6.8	1252	2	O9EDN3	O9EDN3 homo sapien
461	117.5	7.0	1302	1	NRG_DHOME	P20241 drosophila	534	115.5	6.8	1255	2	O7J3Z9	O7J3Z9 homo sapien
462	117.5	7.0	1389	2	O902G9	O902G9 brachydantio	535	115.5	6.8	1255	2	O7YOL8	O7Yol8 pan troglod
463	117.5	7.0	2008	2	O9VEJ5	O9VEJ5 drosophila	536	115.5	6.8	1257	1	CAML_HUMAN	P32004 homo sapien
464	117.5	7.0	2046	2	O7KSG9	O7KSG9 drosophila	537	115.5	6.8	1493	1	NEO1_MOUSE	P97798 mus musculus
465	117.5	7.0	2046	2	AA565164	AA565164 drosophi	538	115.5	6.8	4001	2	O9N2F7	O9N2F7 drosophila
466	117.5	7.0	8625	2	O86GD6	O86GD6 procambiarus	539	115.5	6.8	4796	2	O9N055	O9N055 drosophila
467	117	6.9	351	2	O6WEB2	O6WEB2 branchiost	540	115.5	6.8	4796	2	O9N188	O9N188 drosophila
468	117	6.9	351	2	AAO57589	AAO57589 branchios	541	115.5	6.8	16215	2	O9NFS3	O9Nf3 drosophila
469	117	6.9	401	2	O7PSS8	O7PSS8 anopheles g	542	115.5	6.8	17903	2	O7RTL4	O7RTL4 drosophila

543	115.5	6.8	18074	2	O917U4	O917u4 drosophila	616	113.5	6.7	530	2	O80XJ5	O80xj5 mus musculu
544	115	6.8	217	2	O6KGN0	O6kgno bacterioph	617	113.5	6.7	754	2	O8B276	O8bz76 m mus muscu
545	115	6.8	237	2	O8CG82	O8cg82 mus musculu	618	113.5	6.7	771	2	O7Q3H8	O7qey8 anopheles g
546	115	6.8	294	2	O6KGN1	O6kgn1 bacterioph	619	113.5	6.7	875	2	O912V7	O912v7 mus musculu
547	115	6.8	306	2	O9QYL4	O9qyl4 mus musculu	620	113.5	6.7	939	2	O9VB35	O9vb35 drosophila
548	115	6.8	316	2	O8WBP3	O8wbp3 drosophila	621	113.5	6.7	939	2	O967X6	O967x6 drosophila
549	115	6.8	399	2	O8N772	O8n772 homo sapien	622	113.5	6.7	1248	2	O9XT41	O9xt41 cercopithec
550	115	6.8	424	2	O8C6W0	O8c6w0 mus musculu	623	113.5	6.7	1255	2	O7YQJ7	O7yqj7 pongo pygma
551	115	6.8	602	2	O86Y09	O86y09 homo sapien	624	113.5	6.7	1386	2	ROB3_HUMAN	O86m60 homo sapien
552	115	6.8	650	2	O8NAB4	O8nab4 homo sapien	625	113.5	6.7	1614	2	O8UVD7	O8uvd7 xenopus lae
553	115	6.8	731	2	O8SP16	O8sp16 macroopus eu	626	113.5	6.7	1675	2	O98SM4	O98sm4 brachydanio
554	115	6.8	837	2	O7Z7F2	O7z7f2 homo sapien	627	113	6.7	336	1	C226_HUMAN	O15762 homo sapien
555	115	6.8	1125	2	O7QEC1	O7qec1 anopheles g	628	113	6.7	340	2	O7Q8Q7	O7q8q7 anopheles g
556	115	6.8	1209	1	P702J2	P702j2 mus musculu	629	113	6.7	538	2	O9NMQ7	O9nmq7 homo sapien
557	115	6.8	1302	1	VR2_BRABE	VR2br2 brachydanio	630	113	6.7	1109	2	O6P5H3	O6p5h3 mus musculu
558	115	6.8	1723	2	O8CHB2	O8chb2 mus musculu	631	113	6.7	1109	2	AAH62892	AAH62892 mus muscu
559	115	6.8	2403	2	O8MLD5	O8mld5 drosophila	632	113	6.7	1277	1	CAML_FURRU	O98902 fugu rubrip
560	115	6.8	7210	2	O9V7G8	O9v7g8 drosophila	633	113	6.7	3100	2	O7KYN5	O7kyn5 homo sapien
561	114.5	6.8	163	2	O9NVJ5	O9nvj5 homo sapien	634	113	6.7	4650	2	O15598	O15598 homo sapien
562	114.5	6.8	345	2	O6GN08	O6gn08 xenopus lae	635	112.5	6.7	226	2	O7PYG1	O7pyg1 anopheles g
563	114.5	6.8	363	2	O6NVA1	O6nv41 brachydanio	636	112.5	6.7	244	2	O957B9	O957b9 drosophila
564	114.5	6.8	363	2	AAH68325	AAH68325 brachydan	637	112.5	6.7	338	2	O7Z3W6	O7z3w6 homo sapien
565	114.5	6.8	412	2	O8HY14	O8hy14 cryocolagus	638	112.5	6.7	345	1	OPCM_HUMAN	O14982 homo sapien
566	114.5	6.8	458	2	O61351	O61351 mus musculu	639	112.5	6.7	362	2	O9JHQ1	O9jhg1 rattus norv
567	114.5	6.8	479	2	CAG33099	Cag33099 homo sapi	640	112.5	6.7	363	2	O46147	O46147 onchocerca
568	114.5	6.8	489	2	O7PGL7	O7pgl7 anopheles g	641	112.5	6.7	401	2	O08835	O08835 cercopithec
569	114.5	6.8	497	2	O9BXN7	O9bxn7 homo sapien	642	112.5	6.7	440	2	O6ZMD4	O6zmd4 homo sapien
570	114.5	6.8	499	1	SIL8_HUMAN	O9nyz4 homo sapien	643	112.5	6.7	440	2	BAD1.8794	BAD18794 homo sapi
571	114.5	6.8	504	2	O8N441	O8n441 homo sapien	644	112.5	6.7	517	1	PVR1_HUMAN	O15223 homo sapien
572	114.5	6.8	504	2	O9HAD7	O9had7 homo sapien	645	112.5	6.7	743	2	O6R6B2	O6r6b2 vibrionphage
573	114.5	6.8	504	2	AAO88670	AAO88670 homo sapi	646	112.5	6.7	743	2	AAH92067	AAH92067 vibrionpha
574	114.5	6.8	521	2	O61352	O61352 mus musculu	647	112.5	6.7	782	2	O61563	O61563 mus musculu
575	114.5	6.8	538	1	PVR2_HUMAN	O92692 homo sapien	648	112.5	6.7	1070	2	O610S1	O610s1 homo sapien
576	114.5	6.8	551	2	O8MSN7	O8msn7 drosophila	649	112.5	6.7	1259	1	CAML_RAT	O05655 rattus norv
577	114.5	6.8	956	2	O9W4T9	O9w4t9 drosophila	650	112.5	6.7	1259	2	O9OY38	O9oy38 mus musculu
578	114.5	6.8	959	2	O9N9Y4	O9ny94 drosophila	651	112.5	6.7	1259	2	AAH56988	AAH56988 mus muscu
579	114.5	6.8	975	2	O97174	O97174 drosophila	652	112.5	6.7	1342	2	O9VP27	O9vp27 drosophila
580	114.5	6.8	1088	1	NCA1_XENLA	P16170 xenopus lae	653	112.5	6.7	1342	2	O9GPP6	O9gpp6 drosophila
581	114.5	6.8	1415	2	O94155	O94155 caenorhabdi	654	112.5	6.7	2029	1	LAR_DRONE	O16621 drosophila
582	114.5	6.8	1415	2	AAB37634	Aab37634 caenorhab	655	112.5	6.7	2029	2	O9VIS8	O9vis8 drosophila
583	114.5	6.8	5604	2	O8W253	O8w253 homo sapien	656	112.5	6.7	2224	2	O9UJL1	O9ujl1 drosophila
584	114	6.8	235	2	O75296	O75296 homo sapien	657	112	6.6	316	2	O8WP94	O8wp94 drosophila
585	114	6.8	337	2	O6DPF2	O6dpf2 mus musculu	658	112	6.6	355	2	O7Z3B1	O7z3b1 homo sapien
586	114	6.8	403	2	O8HY15	O8hy15 lemur catta	659	112	6.6	456	2	O8R5M8	O8r5m8 mus musculu
587	114	6.8	438	2	O9JLB7	O9jlb7 mus musculu	660	112	6.6	590	2	O6P4T5	O6p4t5 mus musculu
588	114	6.8	483	2	O9DBP8	O9dbp8 mus musculu	661	112	6.6	590	2	AAH63257	AAH63257 mus muscu
589	114	6.8	508	2	O8CED8	O8ced8 mus musculu	662	112	6.6	913	2	O8T3B5	O8t3b5 caenorhabdi
590	114	6.8	508	2	O8R007	O8r007 mus musculu	663	112	6.6	928	2	O19128	O19128 caenorhabdi
591	114	6.8	510	2	O9JLB8	O9jlb8 mus musculu	664	112	6.6	946	2	O07153	O07153 torpido cal
592	114	6.8	544	1	ICAJ3_BOVIN	O82123 bos taurus	665	112	6.6	955	2	O8WQ86	O8wq86 caenorhabdi
593	114	6.8	545	2	O9VCT4	O9vct4 drosophila	666	112	6.6	1212	2	O95TG0	O95tg0 drosophila
594	114	6.8	672	2	O81P70	O81p70 drosophila	667	112	6.6	1269	2	O01632	O01632 caenorhabdi
595	114	6.8	672	2	AAQ23561	AAQ23561 drosophila	668	112	6.6	1273	2	O44928	O44928 caenorhabdi
596	114	6.8	795	2	O90YMO	O90ymo brachydanio	669	112	6.6	1386	2	O8T172	O8t172 methanogarc
597	114	6.8	1028	2	O8C6X1	O8c6x1 mus musculu	670	111.5	6.6	267	2	O8NC05	O8nc05 homo sapien
598	114	6.8	1028	2	O9JMB8	O9jmb8 mus musculu	671	111.5	6.6	350	2	O95K13	O95k13 macaca fasc
599	114	6.8	1045	2	O86T37	O86t37 homo sapien	672	111.5	6.6	400	1	HPL4_MOUSE	O80wm4 mus musculu
600	114	6.8	1073	2	O9TXI8	O9txi8 caenorhabdi	673	111.5	6.6	508	2	O96L45	O96l45 homo sapien
601	114	6.8	1177	2	O6GXH1	O6gxb1 xenopus lae	674	111.5	6.6	421	2	AAQ88499	AAQ88499 homo sapi
602	114	6.8	1320	2	O86TC9	O86tc9 homo sapien	675	111.5	6.6	421	2	O7OJK4	O7ojk4 anopheles g
603	114	6.8	1320	2	O96KFS	O96kfs homo sapien	676	111	6.6	1060	2	O9QZ13	O9qz13 rattus norv
604	114	6.8	1735	2	O7Q916	O7q916 anopheles g	677	111	6.6	283	2	O8K091	O8k091 mus musculu
605	113.5	6.7	232	2	O7PJ18	O7pj18 anopheles g	678	111	6.6	352	2	O6U706	O6u706 homo sapien
606	113.5	6.7	284	2	O9NX42	O9nx42 homo sapien	679	111	6.6	352	2	AAQ88499	AAQ88499 homo sapi
607	113.5	6.7	296	2	O6PU56	O6pu56 homo sapien	680	111	6.6	421	2	O7PV30	O7pv30 anopheles g
608	113.5	6.7	296	2	AAH23317	AAH23317 homo sapi	681	111	6.6	421	2	O7OLK4	O7olk4 anopheles g
609	113.5	6.7	327	2	O961Q7	O961q7 homo sapien	682	111	6.6	474	2	O7PKB3	O7pkb3 cercopithec
610	113.5	6.7	327	2	AAQ89256	AAQ89256 homo sapi	683	111	6.6	527	2	O9ERP7	O9erp7 cricetus
611	113.5	6.7	382	2	O7PSH7	O7psh7 anopheles g	684	111	6.6	593	2	O7Z696	O7z696 homo sapien
612	113.5	6.7	482	2	BAC29175	Bac29175 mus muscu	685	111	6.6	769	2	O8NT15	O8nt15 homo sapien
613	113.5	6.7	499	2	O7Z728	O7z728 homo sapien	686	111	6.6	806	1	FGR3_HUMAN	P22607 homo sapien
614	113.5	6.7	510	2	O96K15	O96k15 homo sapien	687	111	6.6	807	2	O6NY23	O6ny23 brachydanio
615	113.5	6.7	530	1	PVR2_MOUSE	P32507 mus musculu	688	111	6.6	807	2	AAH6766	AAH6766 brachydan

689	11.1	6.6	960	2	Q7PV74	Q7PV74 anopheles g	762	109	6.5	562	2	AA11440	AA11440 brachydian
690	11.1	6.6	1026	2	Q81W2	Q81W2 homo sapien	763	109	6.5	640	2	Q8BSM2	Q8BSM2 mus musculus
691	11.1	6.6	1228	2	Q8MR23	Q8MR23 drosophila	764	109	6.5	646	1	MU18_HUMAN	P43121 homo sapien
692	11.1	6.6	1228	2	AAE58172	AAE58172 drosophila	765	109	6.5	646	2	Q6PHE3	Q6PHE3 homo sapien
693	11.1	6.6	1235	2	Q86BD5	Q86BD5 drosophila	766	109	6.5	646	2	AAH56418	AAH56418 homo sapi
694	11.1	6.6	1235	2	Q9V787	Q9V787 drosophila	767	109	6.5	1106	2	Q8WX93	Q8WX93 homo sapien
695	11.1	6.6	6632	1	UN89_CAEEL	001761 caenorhabdi	768	108.5	6.4	329	2	BAC28982	BAC28982 mus muscu
696	11.1	6.6	8081	2	Q72120	Q72120 caenorhabdi	769	108.5	6.4	345	1	OPCM_BOVIN	P1834 bos taurus
697	110.5	6.5	370	2	Q6MZ03	Q6MZ03 homo sapien	770	108.5	6.4	348	1	KIT0_RAT	Q92018 rattus norv
698	110.5	6.5	370	2	CAE45975	CAE45975 homo sapi	771	108.5	6.4	348	2	Q80224	Q80224 mus musculus
699	110.5	6.5	330	2	Q96AP7	Q96AP7 homo sapien	772	108.5	6.4	416	2	Q7M048	Q7M048 rattus norv
700	110.5	6.5	330	2	Q96T50	Q96T50 homo sapien	773	108.5	6.4	495	2	Q8CHY1	Q8CHY1 homo sapien
701	110.5	6.5	390	2	AAQ88748	AAQ88748 homo sapi	774	108.5	6.4	705	2	Q8CBD3	Q8CBD3 mus musculus
702	110.5	6.5	422	2	Q96PJ3	Q96PJ3 homo sapien	775	108.5	6.4	878	2	Q9UQ22	Q9UQ22 mytilus gal
703	110.5	6.5	513	2	Q00481	Q00481 homo sapien	776	108.5	6.4	1028	2	Q9UQ52	Q9U522 homo sapien
704	110.5	6.5	515	2	Q96BJ5	Q96BJ5 homo sapien	777	108.5	6.4	1114	2	Q9BMV1	Q9BMV1 homo sapien
705	110.5	6.5	515	2	Q96RE0	Q96RE0 homo sapien	778	108.5	6.4	1115	2	Q6UXJ5	Q6UXJ5 homo sapien
706	110.5	6.5	544	2	Q6UXI8	Q6UXI8 homo sapien	779	108.5	6.4	1328	2	AAQ88694	AAQ88694 homo sapi
707	110.5	6.5	544	2	AAQ88703	AAQ88703 homo sapi	780	108.5	6.4	1328	2	Q21043	Q21043 caenorhabdi
708	110.5	6.5	717	2	AAQ88495	AAQ88495 homo sapi	781	108.5	6.4	2000	2	Q97791	Q97791 oryctolagus
709	110.5	6.5	816	2	Q91285	Q91285 pleurodeles	782	108.5	6.4	2169	2	Q8AV58	Q8AV58 gallus gall
710	110.5	6.5	1070	1	PTK7_HUMAN	Q13308 homo sapien	783	108.5	6.4	4203	2	Q955G2	Q955G2 caenorhabdi
711	110.5	6.5	1189	2	Q9P2J2	Q9P2J2 homo sapien	784	108.5	6.4	4219	2	Q9ND87	Q9ND87 caenorhabdi
712	110.5	6.5	1889	2	Q7Q0X2	Q7Q0X2 anopheles g	785	108.5	6.4	4369	2	Q8MXD7	Q8MXD7 caenorhabdi
713	11.0	6.5	218	2	Q6ZMC6	Q6ZMC6 homo sapien	786	108.5	6.4	4447	2	Q8MXD8	Q8MXD8 caenorhabdi
714	11.0	6.5	218	2	BAD18803	BAD18803 homo sapi	787	108.5	6.4	4488	2	Q9TXK2	Q9TXK2 caenorhabdi
715	11.0	6.5	316	2	Q9BXK1	Q9BXK1 homo sapien	788	108.5	6.4	4736	2	Q7Y799	Q7Y799 mytilus gal
716	11.0	6.5	483	2	Q7SX76	Q7SX76 brachydanio	789	108	6.4	173	2	Q9JKD5	Q9JKD5 rattus norv
717	11.0	6.5	636	2	Q22040	Q22040 caenorhabdi	790	108	6.4	286	2	Q4E535	Q4E535 bos taurus
718	11.0	6.5	741	2	Q6RCF4	Q6RCF4 vibrionphage	791	108	6.4	325	2	Q95791	Q95791 homo sapien
719	11.0	6.5	741	2	AAE97631	AAE97631 vibrionphage	792	108	6.4	325	2	Q8HW98	Q8HW98 mus musculus
720	11.0	6.5	815	2	Q8AYP3	Q8AYP3 brachydanio	793	108	6.4	329	2	Q8NM25	Q8NM25 homo sapien
721	11.0	6.5	86	2	Q8NPF5	Q8NPF5 homo sapien	794	108	6.4	334	2	Q819N2	Q819N2 brachylosto
722	11.0	6.5	837	1	NCM2_HUMAN	Q15394 homo sapien	795	108	6.4	354	2	Q8NMQ3	Q8NMQ3 homo sapien
723	11.0	6.5	917	1	ICAE_MOUSE	Q60625 mus musculus	796	108	6.4	376	2	Q90Z71	Q90Z71 brachydanio
724	11.0	6.5	1070	2	Q61Q54	Q61Q54 homo sapien	797	108	6.4	509	2	Q9EQY5	Q9EQY5 mus muscu
725	11.0	6.5	1070	2	AAH04862	AAH04862 homo sapi	798	108	6.4	526	1	BUTY_BOVIN	BUTY_BOVIN
726	11.0	6.5	1070	2	AAH71557	AAH71557 homo sapi	799	108	6.4	614	2	Q6DDQ7	Q6DDQ7 xenopus lae
727	11.0	6.5	1097	1	PGDR_RAT	Q05010 rattus norv	800	108	6.4	868	1	MUSK_RAT	MUSK_RAT
728	11.0	6.5	1378	1	ROB2_HUMAN	Q9HCK4 homo sapien	801	109	6.4	1099	2	P97527	P97527 rattus norv
729	11.0	6.5	1391	2	Q8N3L4	Q8N3L4 homo sapien	802	108	6.4	1150	2	Q8BS24	Q8BS24 mus musculus
730	11.0	6.5	1880	2	Q18465	Q18465 hirtudo medi	803	108	6.4	2325	2	Q9N3X8	Q9N3X8 caenorhabdi
731	11.0	6.5	2399	2	Q6BEO6	Q6BEO6 caenorhabdi	804	107.5	6.4	270	2	BAC26003	BAC26003 mus muscu
732	109.5	6.5	333	2	Q9BDM2	Q9BDM2 cercopitheci	805	107.5	6.4	288	2	BAC29632	BAC29632 mus muscu
733	109.5	6.5	333	1	C226_MOUSE	Q8K4F0 mus musculus	806	107.5	6.4	323	2	Q9BDB8	Q9BDB8 cercopiebus
734	109.5	6.5	334	2	Q819N0	Q819N0 branchiosto	807	107.5	6.4	350	2	Q99420	Q99420 homo sapien
735	109.5	6.5	345	1	OPCM_RAT	P32736 rattus norv	808	107.5	6.4	350	2	Q819N1	Q819N1 branchiosto
736	109.5	6.5	349	1	CEAE_HUMAN	P31997 homo sapien	809	107.5	6.4	366	2	Q8N759	Q8N759 homo sapien
737	109.5	6.5	333	2	Q7QBC5	Q7QBC5 anopheles g	810	107.5	6.4	402	1	HPV4_HUMAN	HPV4_HUMAN
738	109.5	6.5	430	2	Q7QGS8	Q7QGS8 anopheles g	811	107.5	6.4	428	2	Q96PJ6	Q96PJ6 homo sapien
739	109.5	6.5	435	2	Q8N3J6	Q8N3J6 anopheles g	812	107.5	6.4	429	2	Q96LA6	Q96LA6 homo sapien
740	109.5	6.5	477	2	Q6UXJ4	Q6UXJ4 homo sapien	813	107.5	6.4	605	2	Q6CNT9	Q6CNT9 xenopus lae
741	109.5	6.5	477	2	AAQ88696	AAQ88696 homo sapi	814	107.5	6.4	659	2	Q6ZNM1	Q6ZNM1 homo sapien
742	109.5	6.5	526	1	BUTY_HUMAN	Q13410 homo sapien	815	107.5	6.4	659	2	BAC85123	BAC85123 homo sapi
743	109.5	6.5	526	2	Q9H458	Q9H458 homo sapien	816	107.5	6.4	660	2	Q72681	Q72681 homo sapien
744	109.5	6.5	595	2	Q90720	Q90720 gallus gall	817	107.5	6.4	1026	2	Q62845	Q62845 rattus norv
745	109.5	6.5	1336	1	VGR1_RAT	P53767 rattus norv	818	107.5	6.4	1225	2	Q6GPE1	Q6GPE1 xenopus lae
746	109.5	6.5	1465	2	Q7QGS5	Q7QGS5 mus musculus	819	107.5	6.4	1235	2	Q95428	Q95428 homo sapien
747	109	6.5	263	2	Q7TPM5	Q7TPM5 mus musculus	820	107	6.3	199	2	Q8ND10	Q8ND10 homo sapien
748	109	6.5	283	2	Q7TPH5	Q7TPH5 mus musculus	821	107	6.3	332	2	Q6UXG3	Q6UXG3 homo sapien
749	109	6.5	283	2	Q7TSP5	Q7TSP5 mus musculus	822	107	6.3	332	2	AAQ88730	AAQ88730 homo sapi
750	109	6.5	283	2	AAQ24205	AAQ24205 mus muscu	823	107	6.3	437	2	Q8NPF6	Q8NPF6 homo sapien
751	109	6.5	292	2	Q6UY47	Q6UY47 homo sapien	824	107	6.3	442	2	Q6KAT6	Q6KAT6 mus musculus
752	109	6.5	292	2	AAQ88451	AAQ88451 homo sapi	825	107	6.3	442	2	BAD21371	BAD21371 mus muscu
753	109	6.5	316	2	Q8MP58	Q8MP58 drosophila	826	107	6.3	449	2	Q9UEI6	Q9UEI6 homo sapien
754	109	6.5	328	2	Q88775	Q88775 rattus norv	827	107	6.3	515	1	PVRI_MOUSE	PVRI_MOUSE
755	109	6.5	338	2	AAH61846	AAH61846 rattus no	828	107	6.3	515	2	Q6PPM9	Q6PPM9 mus musculus
756	109	6.5	336	2	Q46551	Q46551 hyllobates s	829	107	6.3	515	2	AAH60694	AAH60694 mus muscu
757	109	6.5	345	2	Q7PVU1	Q7PVU1 anopheles g	830	107	6.3	602	2	Q9ESS8	Q9ESS8 rattus norv
758	109	6.5	437	2	Q81ZP8	Q81ZP8 homo sapien	831	107	6.3	622	2	Q9JKB2	Q9JKB2 mus musculus
759	109	6.5	547	1	CD19_MOUSE	P25918 mus musculus	832	107	6.3	648	2	Q9EPF2	Q9EPF2 rattus norv
760	109	6.5	547	1	BAC40973	BAC40973 mus muscu	833	107	6.3	773	1	PIGR_RABIT	P01332 oryctolagus
761	109	6.5	562	2	Q6VYR7	Q6VYR7 brachydanio	834	107	6.3	817	2	Q8UG38	Q8UG38 brachydanio

835	107	6.3	2558	2	06NR91	06nr91 drosophila	908	105	6.2	232	2	08BZ74	08bz74 mus musculus
836	107	6.3	2558	2	AAR8555	Aar8555 drosophila	909	105	6.2	408	2	09VTR3	09vtr3 drosophila
837	107	6.3	19066	2	0801W8	0801w8 brachydanio	910	105	6.2	509	2	091YK7	091yk7 mus musculus
838	106.5	6.3	289	2	09QYLS	09qyls mus musculus	911	105	6.2	533	2	08NCB6	08ncb6 homo sapien
839	106.5	6.3	304	2	09CVA4	09cva4 mus musculus	912	105	6.2	622	2	09RO69	09ro69 mus musculus
840	106.5	6.3	354	1	HPLI_HORSE	028381 equus caball	913	105	6.2	622	2	09ES65	09es65 mus musculus
841	106.5	6.3	437	2	086YV1	086yv1 homo sapien	914	105	6.2	646	2	095812	095812 homo sapien
842	106.5	6.3	546	2	080X70	080x70 mus musculus	915	105	6.2	650	2	099K86	099k86 mus musculus
843	106.5	6.3	548	2	099N33	099n33 mus musculus	916	105	6.2	662	2	08M229	08m229 drosophila
844	106.5	6.3	719	2	09U4G1	09u4g1 drosophila	917	105	6.2	662	2	09VGD0	09vgd0 drosophila
845	106.5	6.3	719	2	AAF51028	Aaf51028 drosophila	918	105	6.2	724	2	003836	003836 xenopus lae
846	106.5	6.3	793	2	070246	070246 mus musculus	919	105	6.2	739	2	0865F2	0865f2 cycetolagus
847	106.5	6.3	813	2	08B0C3	08b0c3 mus musculus	920	105	6.2	800	2	09JHX9	09jhx9 rattus norv
848	106.5	6.3	1227	2	021038	021038 caenorhabdi	921	105	6.2	810	2	09PS96	09ps96 xenopus lae
849	106.5	6.3	1232	2	090284	090284 carassius a	922	105	6.2	828	2	09DGR3	09dgr3 xenopus lae
850	106	6.3	316	2	06UX12	06ux12 homo sapien	923	105	6.2	998	2	0977Y2	0977y2 thermoplasm
851	106	6.3	316	2	AAQ88709	Aaq88709 homo sapi	924	105	6.2	1066	2	08MSR5	08msr5 drosophila
852	106	6.3	317	2	08BEK4	08bek4 ccmox vtru	925	105	6.2	1215	2	07KX17	07kx17 drosophila
853	106	6.3	381	2	08R4B1	08r4b1 mus musculus	926	105	6.2	1215	2	AA664657	AA664657 drosophila
854	106	6.3	407	2	09D234	09d234 mus musculus	927	105	6.2	1461	2	08T9P6	08t9p6 drosophila
855	106	6.3	582	2	080WV2	080wv2 mus musculus	928	105	6.2	1503	2	07KX18	07kx18 drosophila
856	106	6.3	907	2	09NEG0	09neg0 drosophila	929	105	6.2	1503	2	AA564655	AA564655 drosophila
857	106	6.3	919	2	07JPE6	07jpe6 caenorhabdi	930	105	6.2	1509	2	09VLQ8	09vlq8 drosophila
858	106	6.3	919	2	07KXP0	07kxp0 caenorhabdi	931	105	6.2	3215	2	08IRV7	08irv7 drosophila
859	106	6.3	947	2	044171	044171 caenorhabdi	932	105	6.2	4117	2	08IRV9	08irv9 drosophila
860	106	6.3	947	2	026262	026262 caenorhabdi	933	105	6.2	4179	2	09MAY4	09may4 drosophila
861	106	6.3	1040	1	EG15_CABEL	010655 caenorhabdi	934	105	6.2	4223	2	08MPN3	08mpn3 drosophila
862	106	6.3	1051	2	07JL68	07jl68 caenorhabdi	935	105	6.2	4228	2	08IRV8	08irv8 drosophila
863	106	6.3	1051	2	CAE47468	CAe47468 caenorhab	936	105	6.2	4816	2	08T103	08t103 bombyx mori
864	106	6.3	1096	2	08MO14	08mo14 caenorhabdi	937	104.5	6.2	265	2	002280	002280 caenorhabdi
865	106	6.3	1098	1	PGDR_MOUSE	PGe522 mus musculus	938	104.5	6.2	360	2	08MR66	08mr66 drosophila
866	106	6.3	1109	2	08CR51	08ce51 mus musculus	939	104.5	6.2	395	2	08BXJ7	08bxj7 m mus muscu
867	106	6.3	1110	2	08CR73	08ce73 mus musculus	940	104.5	6.2	395	2	08BZP4	08bzp4 mus musculus
868	106	6.3	1409	2	0801M2	0801m2 brachydanio	941	104.5	6.2	417	1	FVR_CERAE	F32506 cercopithec
869	106	6.3	1409	2	08J127	08j127 brachydanio	942	104.5	6.2	430	2	08N4F1	08n4f1 homo sapien
870	106	6.3	1428	2	08AY67	08ay67 brachydanio	943	104.5	6.2	431	2	AAQ88508	AAq88508 homo sapi
871	106	6.3	1474	2	08T4W0	08t4w0 drosophila	944	104.5	6.2	523	2	08K2H7	08k2h7 mus musculus
872	106	6.3	1509	2	08IRP1	08irp1 drosophila	945	104.5	6.2	538	2	09OX07	09ox07 mus musculus
873	106	6.3	1509	2	095P10	095p10 drosophila	946	104.5	6.2	582	2	095N25	095n25 bos taurus
874	106	6.3	1914	1	KML5_HUMAN	015746 homo sapien	947	104.5	6.2	722	2	06GNB3	06gnb3 xenopus lae
875	106	6.3	1914	1	07Z4U0	07z4u0 homo sapien	948	104.5	6.2	920	2	09P232	09p232 homo sapien
876	106	6.3	2222	2	07OEG7	07oeg7 anopheles g	949	104.5	6.2	931	2	06KAM5	06kam5 mus musculus
877	105.5	6.2	318	2	08AYZ8	08ayz8 variola vir	950	104.5	6.2	931	2	BAD21432	Bad21432 mus muscu
878	105.5	6.2	318	2	08BRT5	08bels variola vir	951	104.5	6.2	1184	2	075339	075339 homo sapien
879	105.5	6.2	328	2	09Z109	09z109 mus musculus	952	104.5	6.2	1184	2	06TW99	06tw99 homo sapien
880	105.5	6.2	394	2	06UXG0	06uxg0 homo sapien	953	104.5	6.2	1184	2	AAQ89263	AAq89263 homo sapi
881	105.5	6.2	394	2	AAQ88735	Aaq88735 homo sapien	954	104.5	6.2	1185	2	07PRK4	07prk4 anopheles g
882	105.5	6.2	408	2	08BVP6	08bvp6 mus musculus	955	104.5	6.2	1377	1	NEO1_RAT	NEo1879 ratius norv
883	105.5	6.2	408	2	08K094	08k094 m hypotheci	956	104.5	6.2	1461	1	NEO1_HUMAN	NEo1879 ratius norv
884	105.5	6.2	408	2	091WP1	091wp1 mus musculus	957	104.5	6.2	2222	2	097354	097354 drosophila
885	105.5	6.2	485	1	FODX_RAT	09wqg2 rattus norv	958	104.5	6.2	2230	2	08B607	08b607 drosophila
886	105.5	6.2	525	2	07PZS8	07pzs8 anopheles g	959	104.5	6.2	2230	2	AAQ89028	AAq89028 drosophila
887	105.5	6.2	527	2	06ZTR2	06ztr2 homo sapien	960	104	6.2	299	1	ALC_RABIT	ALc1879 cycetolagus
888	105.5	6.2	527	2	BAC86520	Bac86520 homo sapi	961	104	6.2	307	2	054547	054547 rattus norv
889	105.5	6.2	626	1	MAG_RAT	PO7722 rattus norv	962	104	6.2	307	2	AAH61820	AAh61820 rattus no
890	105.5	6.2	729	2	0638Z7	0638z7 rattus sp.	963	104	6.2	334	2	09NR44	09nr44 homo sapien
891	105.5	6.2	731	2	08CFR8	08cfr8 mus musculus	964	104	6.2	404	2	08B7P1	08b7p1 mus musculus
892	105.5	6.2	733	2	060830	060830 mus musculus	965	104	6.2	524	1	BUTY_MOUSE	BUt2556 mus musculus
893	105.5	6.2	733	2	080T10	080t10 mus musculus	966	104	6.2	524	1	0921K7	0921k7 mus musculus
894	105.5	6.2	789	2	07PME2	07pmez anopheles g	967	104	6.2	600	2	08N7W7	08n7w7 homo sapien
895	105.5	6.2	789	2	08CIM9	08cim9 mus musculus	968	104	6.2	620	2	06IGJ3	06igj3 drosophila
896	105.5	6.2	822	1	FGRI_HUMAN	PI1362 homo sapien	969	104	6.2	694	2	08SWT7	08swt7 drosophila
897	105.5	6.2	822	1	FGRI_MOUSE	PI6092 mus musculus	970	104	6.2	740	2	096F29	096f29 homo sapien
898	105.5	6.2	822	1	FGRI_MOUSE	004589 rattus norv	971	104	6.2	789	2	06X936	06x936 rattus norv
899	105.5	6.2	822	2	AA679322	Aa679322 mus musculi	972	104	6.2	789	2	AAp78673	AAp78673 rattus no
900	105.5	6.2	822	2	AA679322	Aa679322 homo sapi	973	104	6.2	800	2	07TS18	07ts18 mus musculus
901	105.5	6.2	869	1	MUSK_HUMAN	015146 homo sapien	974	104	6.2	801	1	FGR3_MOUSE	FGr1851 mus musculus
902	105.5	6.2	987	2	Q7YZG6	Q7yzm6 caenorhabdi	975	104	6.2	868	2	MUSK_MOUSE	ME1006 mus musculus
903	105.5	6.2	988	2	CAC70094	CaC70094 caenorhab	976	104	6.2	998	2	Q9K4T6	Q9k4t6 drosophila
904	105.5	6.2	1036	2	08SMW3	Q8smw3 drosophila	977	104	6.2	1099	2	07TMR8	Q7tmr8 mus musculus
905	105.5	6.2	1102	2	Q923W7	Q923w7 mus musculus	978	104	6.2	1503	2	08T4L8	Q8t4l8 drosophila
906	105.5	6.2	1390	2	Q9VN14	Q9vn14 drosophila	979	103.5	6.1	147	2	08CFJ3	Q8cfj3 mus musculus
907	105	6.2	145	2	Q9MZE4	Q9mze4 macaca mula	980	103.5	6.1	275	2	Q9BDN9	Q9bdn9 papio anubi

981	103.5	6.1	280	08UWK1	08uwl1	ictalurus p	1054	102	6.0	702	1	CRK5	HUMAN	P06731	homo sapien
982	103.5	6.1	287	2	09QW80	Q9qW80 mus sp. . f	1055	102	6.0	702	2	08N4D0		08n4d0	homo sapien
983	103.5	6.1	329	2	BAC26992	Bac26992 mus muscu	1056	102	6.0	800	2	09J052		09j052	mus musculus
984	103.5	6.1	356	1	HPL1_MOUSE	09qWp78 mus muscu	1057	102	6.0	1030	2	08NF48		08nf48	homo sapien
985	103.5	6.1	376	2	09QW78	09qW78 mus sp. . f	1058	102	6.0	1032	2	08AX24		08ax24	brachydanto
986	103.5	6.1	388	2	08NC34	08nc34 homo sapien	1059	102	6.0	1098	2	0961D6		09e1d6	dtrosophila
987	103.5	6.1	534	2	08NB18	08nb18 homo sapien	1060	102	6.0	1249	2	07RM29		07rm29	rattus norv
988	103.5	6.1	601	2	096CJ3	09e6c3 homo sapien	1061	102	6.0	1271	1	MYPC_CHICK		09m68	gallus gall
989	103.5	6.1	628	1	LU_HUMAN	P50895 homo sapien	1062	102	6.0	1332	2	09QVW7		09qvw7	dtrosophila
990	103.5	6.1	628	1	086VC7	086vc7 homo sapien	1063	102	6.0	1332	2	09BN17		09bn17	dtrosophila
991	103.5	6.1	677	1	NRG1_XENTLA	093383 xenopus lae	1064	102	6.0	1426	2	08GZ11		08gz11	entereococcu
992	103.5	6.1	799	2	08C3V5	08c3v5 mus musculu	1065	101.5	6.0	336	1	C226_MACVU		081906	macaca mla
993	103.5	6.1	799	2	08C1B8	08c1b8 mus musculu	1066	101.5	6.0	413	2	Q26438		Q26438	hyalophora
994	103.5	6.1	819	1	FGRI_CHICK	P21804 gallus gall	1067	101.5	6.0	417	1	PVR_HUMAN		P51511	homo sapien
995	103.5	6.1	824	2	091286	091286 plautodelles	1068	101.5	6.0	417	2	096BJ1		09e6bj1	homo sapien
996	103.5	6.1	940	2	08NFA7	08nf47 homo sapien	1069	101.5	6.0	606	2	Q9YVW6		Q9ymv6	dtrosophila
997	103.5	6.1	998	2	09NR27	09n527 dtrosophila	1070	101.5	6.0	624	2	09ES86		09e866	rattus norv
998	103.5	6.1	1356	1	VGR2_HUMAN	P35968 homo sapien	1071	101.5	6.0	639	2	09ERP30		09erp30	homo sapien
999	103.5	6.1	1513	2	Q90270	Q90270 brachydanto	1072	101.5	6.0	639	2	SIIB_HUMAN		09e16	homo sapien
1000	103.5	6.1	1612	1	ROB1_MOUSE	089026 mus musculu	1073	101.5	6.0	802	2	08TD40		08td40	homo sapien
1001	103.5	6.1	1651	1	ROB1_HUMAN	Q9y6n7 homo sapien	1074	101.5	6.0	829	2	Q9PSV8		Q9psv8	xenopus lae
1002	103.5	6.1	1705	2	Q7PXM9	Q7pxw9 anopheles g	1075	101.5	6.0	898	1	PAS2_SCHAM		P22648	schistocerc
1003	103	6.1	229	2	Q7PUC4	Q7puc4 anopheles g	1076	101.5	6.0	912	1	ICAS_RABIT		Q28730	oryctolagus
1004	103	6.1	415	2	Q60977	Q60977 mus musculu	1077	101.5	6.0	912	1	Q7PVP3		Q7pvp3	mus musculu
1005	103	6.1	498	2	Q8BRT6	Q8btr6 mus musculu	1078	101.5	6.0	1214	2	Q6Z0A6		Q6z0a6	mus musculu
1006	103	6.1	518	2	BAC38136	Bac38136 mus muscu	1079	101.5	6.0	1214	2	BAC97961		BAC97961	mus musculu
1007	103	6.1	583	2	Q7Z5P1	Q7z5p1 homo sapien	1080	101.5	6.0	1250	1	08BV01		08bv01	mus musculu
1008	103	6.1	606	2	Q6IRH8	Q6irh8 rattus norv	1081	101.5	6.0	1260	1	CAML_MOUSE		P11627	mus musculu
1009	103	6.1	606	2	AAH70916	AAH70916 rattus no	1082	101	6.0	298	2	Q9GL74		Q9gl74	cercopithec
1010	103	6.1	702	2	Q80W67	Q80w67 rattus norv	1083	101	6.0	300	2	Q8BEK0		Q8bek0	comopox viru
1011	103	6.1	708	2	Q6UWL6	Q6uwl6 homo sapien	1084	101	6.0	507	2	Q96K90		Q96k90	homo sapien
1012	103	6.1	708	2	AAQ89102	AAQ89102 homo sapi	1085	101	6.0	584	2	Q90989		Q90989	gallus gall
1013	103	6.1	763	2	Q95YM9	Q95ym9 halocynthia	1086	101	6.0	605	2	08RTB0		08rtb0	homo sapien
1014	103	6.1	773	2	AAI27285	AAI27285 dtrosophila	1087	101	6.0	606	2	08C134		08c134	mus musculu
1015	103	6.1	873	1	PAS2_DROME	P34082 dtrosophila	1088	101	6.0	620	1	SNP_COTUA		Q92314	coccurnix co
1016	103	6.1	986	2	Q6DGI7	Q6dgi7 brachydanto	1089	101	6.0	626	2	Q90680		Q90680	gallus gall
1017	103	6.1	1388	2	Q7QKQ0	Q7qkd0 anopheles g	1090	101	6.0	673	2	Q6WZM2		Q6wzm2	homo sapien
1018	103	6.1	1470	1	ROB2_MOUSE	Q7tpd3 mus musculu	1091	101	6.0	673	2	CAE45915		Q9eup1	homo sapien
1019	103	6.1	2633	2	Q8ISF3	Q8isf3 caenorhabdi	1092	101	6.0	693	2	Q9PUP1		Q9t7suv	mus musculu
1020	103	6.1	2708	2	Q8ISF4	Q8isf4 caenorhabdi	1093	101	6.0	700	2	Q7TSUV		BAC333658	mus musculu
1021	103	6.1	2808	2	Q8MNS1	Q8mns1 caenorhabdi	1094	101	6.0	700	2	BAC333658		Q6P1W7	homo sapien
1022	103	6.1	6328	2	Q8MNS0	Q8mns0 caenorhabdi	1095	101	6.0	743	2	Q6P1W7		AAH11846	homo sapi
1023	103	6.1	18519	2	Q8ISF6	Q8isf6 caenorhabdi	1096	101	6.0	743	2	AAH11846		AAH64986	homo sapi
1024	103	6.1	18534	2	Q8ISF7	Q8isf7 caenorhabdi	1097	101	6.0	743	2	Q80W68		Q91287	pleurodeles
1025	102.5	6.1	318	2	Q8BEI6	Q8bei6 variola vir	1098	101	6.0	789	2	Q80W68		Q91287	pleurodeles
1026	102.5	6.1	318	2	Q9QNG4	Q9qng4 variola mln	1099	101	6.0	796	2	Q91287		Q91287	pleurodeles
1027	102.5	6.1	354	1	HPL1_RAT	P03394 rattus norv	1100	101	6.0	890	1	TYO3_HUMAN		Q86VR3	homo sapien
1028	102.5	6.1	356	2	Q8I9K2	Q8i9k2 brachyosteo	1101	101	6.0	890	2	Q86VR3		P57097	rattus norv
1029	102.5	6.1	399	2	Q7QCH7	Q7qch7 anopheles g	1102	101	6.0	994	1	MYRK_RAT		Q75054	homo sapien
1030	102.5	6.1	413	2	Q27418	Q27418 manduca sex	1103	101	6.0	1214	2	Q75054		Q24463	dtrosophila
1031	102.5	6.1	662	2	Q60926	Q60926 homo sapien	1104	101	6.0	1742	2	Q24463		Q24463	dtrosophila
1032	102.5	6.1	992	2	Q9C0L5	Q9c0l5 homo sapien	1105	101	6.0	6048	2	Q7JN85		Q7jns5	caenorhabdi
1033	102.5	6.1	1176	1	KMLS_BOVIN	Q28824 bos taurus	1106	101	6.0	6839	2	Q23350		CA98064	caenorhab
1034	102.5	6.1	1184	2	Q81YI5	Q81yis homo sapien	1107	101	6.0	6839	2	CA98064		CA98081	caenorhab
1035	102.5	6.1	1651	1	ROB1_RAT	Q55005 rattus norv	1108	101	6.0	6839	2	CA98081		Q23551	caenorhabdi
1036	102	6.0	305	2	Q6Z695	Q6z695 homo sapien	1109	101	6.0	7158	2	Q23551		Q8UW11	ictalurus p
1037	102	6.0	305	2	BAC87059	Bac87059 homo sapi	1110	100.5	6.0	280	2	Q9BDM9		Q9bwm9	macaca neme
1038	102	6.0	314	2	Q8BEK8	Q8bek8 vaccinia vi	1111	100.5	6.0	323	2	Q9BDM9		Q9bzm9	macaca neme
1039	102	6.0	319	2	Q00477	Q00477 homo sapien	1112	100.5	6.0	333	2	Q90Z41		Q6GLZ7	gallus gall
1040	102	6.0	332	2	Q9UB81	Q9ub81 homo sapien	1113	100.5	6.0	337	2	Q6GLZ7		Q6s127	xenopus lae
1041	102	6.0	332	2	Q8TA95	Q8ta95 homo sapien	1114	100.5	6.0	355	1	HPL1_CHICK		P07354	gallus gall
1042	102	6.0	332	2	AAH02832	AAH02832 homo sapi	1115	100.5	6.0	430	2	Q800Y8		Q800y8	brachydanto
1043	102	6.0	332	2	AAH20214	AAH20214 homo sapi	1116	100.5	6.0	413	1	HEMO_HYACE		P25033	hyalophora
1044	102	6.0	334	2	Q76PDA0	Q76pda0 homo sapien	1117	100.5	6.0	455	2	Q9UIT0		Q9uit0	homo sapien
1045	102	6.0	350	2	Q8W624	Q8w624 dtrosophila	1118	100.5	6.0	606	2	Q9ES67		Q9es67	mus musculu
1046	102	6.0	357	2	Q15338	Q15338 homo sapien	1119	100.5	6.0	648	2	Q9EPF1		Q9epf1	mus musculu
1047	102	6.0	359	2	P78410	P78410 homo sapien	1120	100.5	6.0	700	1	MEPB_HUMAN		P22480	homo sapien
1048	102	6.0	504	2	Q6NNM1	Q6nnal dtrosophila	1121	100.5	6.0	802	1	FOR4_HUMAN		P22480	homo sapien
1049	102	6.0	504	2	AA96184	AA96184 dtrosophila	1122	100.5	6.0	814	2	Q8EC41		Q8ec41	shewanelia
1050	102	6.0	508	2	Q9VGD2	Q9vgd2 dtrosophila	1123	100.5	6.0	847	1	CB22_HUMAN		P20273	homo sapien
1051	102	6.0	605	2	Q96T84	Q96t84 homo sapien	1124	100.5	6.0	906	2	Q8TFP3		Q8tfp3	mechanosarc
1052	102	6.0	626	1	MAG_MOUSE	P25017 mus musculu	1125	100.5	6.0	1250	2	Q88971		Q88971	mus musculu
1053	102	6.0	664	2	Q9VGD3	Q9vgd3 dtrosophila	1126	100	5.9	307	2	Q94431		Q94431	clona intes

1127	100	5.9	314	2	Q8BEK7	Q8BEK7 vaccinia vi	1200	98.5	5.8	285	2	Q7ZY30	Q7ZY30 xenopus lae
1128	100	5.9	322	1	ICOL_MOUSE	Q9JH18 mus musculu	1201	98.5	5.8	288	2	Q223B5	Q223B5 caenorhabdi
1129	100	5.9	332	2	BAC30938	Bac30938 mus,muscu	1202	-98.5	5.8	309	2	O2YN57	O2YN57 vaccinia vi
1130	100	5.9	354	1	HPL1_HUMAN	P10915 homo sapien	1203	98.5	5.8	316	2	Q7Q0P9	Q7Q0P9 anopheles g
1131	100	5.9	404	2	O8BLQ9	O8BLQ9 mus musculu	1204	98.5	5.8	327	2	O6PCB8	O6PCB8 homo sapien
1132	100	5.9	468	1	CD4_PANTR	P16004 pan troglod	1205	98.5	5.8	327	2	AAH59398	AAH59398 homo sapi
1133	100	5.9	504	2	O98523	O98523 gallus galli	1206	98.5	5.8	413	1	HEMO_MANSE	P31398 manduca sex
1134	100	5.9	527	2	BAC32687	Bac32687 mus muscu	1207	98.5	5.8	482	2	O741A5	O741A5 mycobacteri
1135	100	5.9	584	2	O98921	O98921 gallus galli	1208	98.5	5.8	482	2	AA503504	AA503504 mycobacte
1136	100	5.9	592	2	O9JLMS	O9JLMS mus musculu	1209	98.5	5.8	493	2	O6PSY4	O6PSY4 homo sapien
1137	100	5.9	626	2	O98922	O98922 gallus galli	1210	98.5	5.8	493	2	AAH62581	AAH62581 homo sapi
1138	100	5.9	654	2	Q78BGI	Q78BGI neurospora	1211	98.5	5.8	525	2	Q7QJX5	Q7QJX5 anopheles g
1139	100	5.9	784	2	O81063	O81063 dirosophila	1212	98.5	5.8	548	2	Q9Z1J3	Q9Z1J3 ractus novr
1140	100	5.9	807	2	O6DDE6	O6DDE6 xenopus lae	1213	98.5	5.8	602	1	NRG1_CHICK	Q005199 gallus galli
1141	100	5.9	818	1	TRKB_CHICK	Q91987 gallus galli	1214	98.5	5.8	611	2	O8CVC7	O8CVC7 streptococc
1142	100	5.9	848	2	O9PSV7	O9PSV7 xenopus lae	1215	98.5	5.8	648	2	O8R2Y2	O8R2Y2 mus musculu
1143	100	5.9	866	2	O57577	O57577 cynops pyr	1216	98.5	5.8	1005	2	P79921	P79921 xenopus lae
1144	100	5.9	1026	2	O94780	O94780 homo sapien	1217	98.5	5.8	1014	2	Q6NPK6	O6NPK6 homo sapien
1145	100	5.9	1100	2	O94779	O94779 homo sapien	1218	98.5	5.8	1021	2	P79757	P79757 gallus galli
1146	100	5.9	1100	2	O57576	O57576 cynops pyr	1219	98.5	5.8	1333	1	VR1_MOUSE	P335969 mus musculu
1147	100	5.9	1180	2	O8T157	O8T157 methanobarc	1220	98	5.8	299	2	Q7Q863	Q7Q863 anopheles g
1148	99.5	5.9	295	2	O9GL75	O9GL75 bos taurus	1221	98	5.8	347	2	O9H730	O9H730 homo sapien
1149	99.5	5.9	323	2	O9BDM4	O9BDM4 macaca mula	1222	98	5.8	394	2	O8HXK9	O8HXK9 macaca fasci
1150	99.5	5.9	416	2	O96360	O96360 hyphancrtria	1223	98	5.8	394	2	O8HXK9	O8HXK9 macaca mula
1151	99.5	5.9	432	2	O6DDE7	O6DDE7 xenopus lae	1224	98	5.8	413	2	O8BG84	O8BG84 m mus musculu
1152	99.5	5.9	459	1	CD4_RABYT	P46630 onycoclaqus	1226	98	5.8	443	2	O8N2P4	O8N2P4 homo sapien
1153	99.5	5.9	549	2	O6PFC5	O6PFC5 mus musculu	1226	98	5.8	500	2	O6UXK1	O6UXK1 homo sapien
1154	99.5	5.9	549	2	AAH57628	AAH57628 mus muscu	1227	98	5.8	589	2	AAO88887	AAO88887 homo sapi
1155	99.5	5.9	549	2	BAC31895	Bac31895 m adult r	1228	98	5.8	640	2	O8R366	O8R366 mus musculu
1156	99.5	5.9	549	2	BAC32002	Bac32002 m adult r	1229	98	5.8	640	2	O8BG88	O8BG88 m mus muscu
1157	99.5	5.9	626	1	MAG_HUMAN	P20916 homo sapien	1230	98	5.8	640	2	O8C031	O8C031 mus musculu
1158	99.5	5.9	876	2	Q7PM78	Q7PM78 anopheles g	1231	98	5.8	697	1	Q8N475	Q8N475 homo sapien
1159	99.5	5.9	1009	2	O8BKU6	O93250 xenopus lae	1232	98	5.8	847	2	O8N475	O8N475 homo sapien
1160	99.5	5.9	1019	2	O8BKU6	O8BKU6 mus musculu	1233	98	5.8	850	2	O9JLF7	O9JLF7 homo sapien
1161	99.5	5.9	1028	2	O62682	O62682 ractus novr	1234	98	5.8	880	1	TTQ3_MOUSE	P55144 mus musculu
1162	99.5	5.9	1031	2	O80YN7	O80YN7 mus musculu	1235	98	5.8	880	1	TTQ3_RAT	P55146 ractus novr
1163	99.5	5.9	1256	2	O9JIX1	O9JIX1 mus musculu	1236	98	5.8	880	2	O6NZM6	O6NZM6 mus musculu
1164	99.5	5.9	1379	2	P79701	P79701 coturnix co	1237	98	5.8	881	2	AAH66058	AAH66058 mus muscu
1165	99.5	5.9	1450	2	Q7QCP2	Q7QCP2 anopheles g	1238	98	5.8	931	2	O7T225	O7T225 gallus galli
1166	99.5	5.9	1569	2	O6PAC0	O6PAC0 mus musculu	1239	98	5.8	939	2	O9VH85	O9VH85 dirosophila
1167	99.5	5.9	1569	2	AAH60378	AAH60378 mus muscu	1240	98	5.8	945	2	O77589	O77589 equus caball
1168	99.5	5.9	1666	1	MYM1_MOUSE	Q62234 mus musculu	1241	98	5.8	1021	2	O93033	O93033 homo sapien
1169	99.5	5.9	1666	1	CAB46494	Cab46494 mus muscu	1242	98	5.8	1252	2	O9JLJ1	O9JLJ1 mus musculu
1170	99	5.9	234	2	O8IZQ9	O8IZQ9 homo sapien	1243	98	5.8	1499	2	O9O815	O9O815 gallus galli
1171	99	5.9	275	1	V055_FOWPV	P21975 fowllox vir	1244	98	5.8	1896	2	O9JAI1	O9JAI1 xenopus lae
1172	99	5.9	275	2	O70H56	O70H56 fowllox vir	1245	97.5	5.8	210	2	O7PVU9	O7PVU9 anopheles g
1173	99	5.9	275	2	CAE52600	CAE52600 Fowllox v	1246	97.5	5.8	257	2	O6NMW2	O6NMW2 brachydantio
1174	99	5.9	313	1	O89197	O89197 varitola vir	1247	97.5	5.8	257	2	AAH67677	AAH67677 brachydan
1175	99	5.9	359	2	HPL3_MOUSE	O6U0M5 mus musculu	1248	97.5	5.8	261	2	O9M6V1	O9M6V1 gallus galli
1176	99	5.9	458	1	CD4_HUMAN	P01730 homo sapien	1249	97.5	5.8	262	2	O8OT70	O8OT70 mus musculu
1177	99	5.9	478	2	BAC50000	Bac5000 m 13 days	1250	97.5	5.8	313	2	O9OZ31	O9OZ31 brachydantio
1178	99	5.9	520	2	O7Z3M6	O7Z3M6 homo sapien	1251	97.5	5.8	354	2	O8BEX1	O8BEX1 compox vitru
1179	99	5.9	542	2	O8NHNS	O8NHNS homo sapien	1252	97.5	5.8	354	1	HPL1_BOVIN	P55252 bos taurus
1180	99	5.9	584	2	O00478	O00478 homo sapien	1253	97.5	5.8	354	1	HPL1_PIG	P10859 sus scrofa
1181	99	5.9	633	2	O7Z5P2	O7Z5P2 homo sapien	1254	97.5	5.8	418	2	O9EPN5	O9EPN5 hydrachoerua
1182	99	5.9	734	2	O96L44	O96L44 homo sapien	1255	97.5	5.8	423	2	O9WRU4	O9WRU4 macaca mula
1183	99	5.9	734	2	O96P31	O96P31 homo sapien	1256	97.5	5.8	510	2	O6EH12	O6EH12 ractus novr
1184	99	5.9	742	2	O8N6S2	O8N6S2 homo sapien	1257	97.5	5.8	534	2	O86S84	O86S84 homo sapien
1185	99	5.9	756	2	O80020	O80020 brachydantio	1258	97.5	5.8	457	2	O66672	O66672 pan troglod
1186	99	5.9	773	2	O9NSW7	O9NSW7 homo sapien	1259	97.5	5.8	473	2	O83HS2	O83HS2 tropheryma
1187	99	5.9	789	2	O8C5U9	O8C5U9 mus musculu	1260	97.5	5.8	476	2	O8OWT0	O8OWT0 mus musculu
1188	99	5.9	812	1	FGRL_XENILA	P22182 xenopus lae	1261	97.5	5.8	510	2	O6EH12	O6EH12 ractus novr
1189	99	5.9	818	2	O91752	O91742 xenopus lae	1262	97.5	5.8	534	2	O86S84	O86S84 homo sapien
1190	99	5.9	831	2	O718Y9	O718Y9 gallus galli	1263	97.5	5.8	534	2	O66672	O66672 pan troglod
1191	99	5.9	831	2	AAQ14282	AAQ14282 gallus ga	1264	97.5	5.8	764	1	TCR_DRONE	O08180 dirosophila
1192	99	5.9	862	1	CD22_MOUSE	P35329 mus musculu	1265	97.5	5.8	764	2	O8MQ01	O8MQ01 dirosophila
1193	99	5.9	997	2	O7PKX0	O7PKX0 anopheles g	1266	97.5	5.8	821	1	TRKB_MOUSE	P15209 mus musculu
1194	99	5.9	1011	2	BAC32470	Bac32470 m adult m	1267	97.5	5.8	821	1	TRKB_MOUSE	P15209 mus musculu
1195	99	5.9	1375	2	O94537	O94537 dirosophila	1268	97.5	5.8	876	2	O78B87	O78B87 mus musculu
1196	99	5.9	1526	2	O94538	O94538 dirosophila	1269	97.5	5.8	931	2	O95185	O95185 homo sapien
1197	99	5.9	3197	2	O9WIDS	O9WIDS dirosophila	1270	97.5	5.8	931	2	O8YAJ7	O8YAJ7 listeria mo
1198	98.5	5.8	279	2	O9UD50	O9UD50 homo sapien	1271	97.5	5.8	1443	1	NBO1_CHICK	O90610 gallus galli
1199	98.5	5.8	283	2	Q7QGT4	Q7QGT4 anopheles g	1272	97	5.7	240	2	O8WU3	O8WU3 homo sapien

1273	97	5.7	279	2	Q7TST0	Q7tst0 mus musculu	1346	96	5.7	612	2	Q8BQ05	Q8bq05 m mus muscu
1274	97	5.7	280	2	Q8UW12	Q8uw12 ictalurus p	1347	96	5.7	619	2	Q7PX10	Q7px10 anopheles g
1275	97	5.7	304	2	Q9BE26	Q9be26 macaca fasc	1348	96	5.7	636	2	Q7LON3	Q7lon3 homo sapien
1276	97	5.7	305	2	Q7PR66	Q7pr66 anopheles g	1349	96	5.7	636	2	AAH41374	Aah41374 homo sapi
1277	97	5.7	307	2	Q66607	Q66607 equid herpe	1350	96	5.7	639	1	NRG1_HUMAN	Q02297 h pro-neure
1278	97	5.7	310	2	Q8BB18	Q8be18 vaccinia vl	1351	96	5.7	640	2	Q7RTV8	Q7rtv8 homo sapien
1279	97	5.7	317	2	Q8BER2	Q8ber2 compox viru	1352	96	5.7	640	2	Q9HCJ2	Q9hcj2 homo sapien
1280	97	5.7	333	2	Q8HXR8	Q8hxr8 cercopithec	1353	96	5.7	640	2	AAQ86660	Aaq86660 homo sapi
1281	97	5.7	456	1	Q7PUM9	Q7pum9 anopheles g	1354	96	5.7	650	1	LIB1_HUMAN	Q8n16 h leukocyte
1282	97	5.7	485	2	A1BG_HUMAN	P04217 homo sapien	1355	96	5.7	739	1	VCA1_MOUSE	P29533 mus musculu
1283	97	5.7	637	2	Q8TC35	Q8tc35 homo sapien	1356	96	5.7	739	2	Q91X98	Q91x98 mus musculu
1284	97	5.7	724	2	Q8MXU5	Q8mxu5 caenorhabdi	1357	96	5.7	766	2	Q810H3	Q810h3 mus musculu
1285	97	5.7	739	1	VCA1_HUMAN	P19320 homo sapien	1358	96	5.7	802	2	Q95M13	Q95m13 bos taurus
1286	97	5.7	739	2	Q6NUJ8	Q6nuj8 homo sapien	1359	96	5.7	1016	2	Q7JFL6	Q7jfl6 oncotrypanu
1287	97	5.7	751	2	Q39294	Q39294 equine herp	1360	96	5.7	1145	2	Q9BKL8	Q9bkl8 aplysia cal
1288	97	5.7	778	2	AAH6490	Aah6490 homo sapi	1361	96	5.7	1193	2	Q9YQW1	Q9yqw1 drosophila
1289	97	5.7	824	2	Q90749	Q90749 gallus gall	1362	96	5.7	1252	2	Q9E0S9	Q9e0s9 mus musculu
1290	97	5.7	931	2	Q8NF26	Q8nf26 homo sapien	1363	96	5.7	1253	2	Q9E0S8	Q9e0s8 mus musculu
1291	97	5.7	949	1	MDCL_RAT	P60756 rattus norv	1364	96	5.7	1294	2	Q80TB0	Q80tb0 mus musculu
1292	97	5.7	1028	2	Q07409	Q07409 mus musculu	1365	96	5.7	1330	2	Q8Y479	Q8y479 listeria mo
1293	97	5.7	1147	1	KMLS_RABIT	P29284 oncotrypanu	1366	96	5.7	1744	2	Q8ZYW8	Q8zyw8 enterococcu
1294	97	5.7	1273	2	Q6R2F7	Q6r2f7 homo sapien	1367	96	5.7	6875	2	Q28733	Q28733 oncotrypanu
1295	97	5.7	1273	2	AAH89909	Aah89909 homo sapi	1368	95.5	5.7	220	2	Q7PX67	Q7px67 anopheles g
1296	97	5.7	1274	1	MYPC_HUMAN	Q14836 homo sapien	1369	95.5	5.7	243	1	CD48_HUMAN	P09326 homo sapien
1297	97	5.7	1274	2	Q9UM53	Q9um53 homo sapien	1370	95.5	5.7	243	2	Q61A22	Q61a22 homo sapien
1298	97	5.7	1345	2	Q8VCD0	Q8vcd0 mus musculu	1371	95.5	5.7	243	2	CAG33293	Cag33293 homo sapi
1299	97	5.7	1367	1	VGR2_MOUSE	P35918 mus musculu	1372	95.5	5.7	308	2	Q60VZ1	Q60vz1 aracetaba v
1300	97	5.7	1535	2	Q21951	Q23991 drosophila	1373	95.5	5.7	308	2	Q91ZR9	Q91zr9 caratagalo o
1301	97	5.7	1860	2	Q7PQF4	Q7pqf4 anopheles g	1374	95.5	5.7	308	2	AA809951	Aa809951 aracetaba
1302	97	5.7	6620	2	Q96AA2	Q96aa2 homo sapien	1375	95.5	5.7	416	2	Q9NPP6	Q9npp6 homo sapien
1303	96.5	5.7	187	2	Q8KA84	Q8ka84 mus musculu	1376	95.5	5.7	611	2	Q9H9N1	Q9h9n1 homo sapien
1304	96.5	5.7	133	2	Q7QGT6	Q7qgt6 anopheles g	1377	95.5	5.7	671	2	Q70W32	Q70w32 oncotrypanu
1305	96.5	5.7	313	2	Q85400	Q85400 macaca mula	1378	95.5	5.7	692	1	CAD58653	Cad58653 oncotrypanu
1306	96.5	5.7	332	2	Q8AYZ7	Q8ayz7 variola maj	1379	95.5	5.7	757	2	Q800Y9	Q800y9 brachydanio
1307	96.5	5.7	385	2	Q9K6V2	Q9k6v2 gallus gall	1380	95.5	5.7	757	2	Q7QCU0	Q7qcu0 anopheles g
1308	96.5	5.7	404	2	Q9YJ39	Q9yjd5 homo sapien	1381	95.5	5.7	879	2	Q8V199	Q8v199 rattus norv
1309	96.5	5.7	423	2	Q9JZM8	Q9jzm8 macaca mula	1382	95.5	5.7	888	2	Q8V1A0	Q8v1a0 rattus norv
1310	96.5	5.7	510	2	Q7L3E0	Q7l3e0 homo sapien	1383	95.5	5.7	891	1	Q8BRX1	Q8brx1 mus musculu
1311	96.5	5.7	510	2	AAH13867	Aah13867 homo sapi	1384	95.5	5.7	1131	1	MYPE_CHICK	P16419 gallus gall
1312	96.5	5.7	571	2	Q8SPI8	Q8spi8 sus scrofa	1385	95.5	5.7	1163	2	Q7XG19	Q7xg19 oryza sativ
1313	96.5	5.7	537	2	Q8IUT0	Q8iut0 homo sapien	1386	95.5	5.7	1163	2	Q94HMS	Q94hms oryza sativ
1314	96.5	5.7	733	2	Q8SQJ3	Q8sqj3 trichosurus	1387	95.5	5.7	1242	1	NPHN_MOUSE	Q9qz87 mus musculu
1315	96.5	5.7	772	2	Q9YJZ6	Q9y216 homo sapien	1388	95.5	5.7	1264	1	P91767	P91767 manduca sex
1316	96.5	5.7	777	2	Q6P555	Q6p555 mus musculu	1389	95.5	5.7	1948	1	PTNS_HUMAN	Q13332 homo sapien
1317	96.5	5.7	777	2	AAH63072	Aah63072 mus muscu	1390	95	5.6	181	2	Q91655	Q91655 xenopus lae
1318	96.5	5.7	778	2	Q8BR86	Q8br86 mus musculu	1391	95	5.6	229	2	Q7PVL3	Q7pvl3 anopheles g
1319	96.5	5.7	782	2	Q9BSA5	Q9bas5 rattus norv	1392	95	5.6	252	2	Q9CK63	Q9ck63 mus musculu
1320	96.5	5.7	800	2	Q86LP9	Q86lf9 drosophila	1393	95	5.6	270	2	Q00426	Q00426 homo sapien
1321	96.5	5.7	801	2	Q86LP8	Q86lf8 drosophila	1394	95	5.6	312	2	Q8BEJ3	Q8bej3 rabbitipox v
1322	96.5	5.7	804	2	Q800Z1	Q800z1 brachydanio	1395	95	5.6	438	2	Q920C3	Q920c3 mus musculu
1323	96.5	5.7	806	2	Q90Z00	Q90z00 brachydanio	1396	95	5.6	457	2	Q96OD1	Q96od1 drosophila
1324	96.5	5.7	1200	1	HYAL_STRPU	Q76536 strigylloce	1397	95	5.6	521	1	C166_RABIT	Q46651 oncotrypanu
1325	96.5	5.7	1232	2	Q8TCG8	Q8tcg8 homo sapien	1398	95	5.6	591	2	Q9UQJ3	Q9uqj3 homo sapien
1326	96.5	5.7	1560	1	TEYN_MOUSE	Q80271 mus musculu	1399	95	5.6	601	2	Q86X29	Q86x29 homo sapien
1327	96.5	5.7	2013	2	Q8Y9T8	Q8y9t8 listeria mo	1400	95	5.6	814	2	Q81VU1	Q81vu1 homo sapien
1328	96.5	5.7	238	2	Q9UBG8	Q9ubg8 manduca sex	1401	95	5.6	814	2	Q91897	Q91897 xenopus lae
1329	96.5	5.7	238	2	Q7PVK5	Q7pvk5 anopheles g	1402	95	5.6	847	2	AAH67107	Aah67107 homo sapi
1330	96	5.7	224	2	Q9MCS7	Q9mc7 bacterioph	1403	95	5.6	847	2	Q8CPR2	Q8cpr2 m mus muscu
1331	96	5.7	236	2	Q6P5S3	Q6p5s3 homo sapien	1404	95	5.6	879	2	Q8C4T3	Q8c4t3 mus musculu
1332	96	5.7	236	2	AAH62711	Aah62711 homo sapi	1405	95	5.6	879	1	FPKP_MOUSE	Q9wv91 mus musculu
1333	96	5.7	252	2	Q8ML12	Q8ml12 drosophila	1406	95	5.6	944	1	MDCL_MOUSE	Q62786 rattus norv
1334	96	5.7	293	2	AAH38070	Aah38070 mus muscu	1407	95	5.6	999	1	Q9VBE5	Q9vbe5 mus musculu
1335	96	5.7	310	2	Q7OK35	Q7ok35 anopheles g	1408	95	5.6	994	1	MERR_MOUSE	Q60805 mus musculu
1336	96	5.7	310	2	Q7TO98	Q7tq98 mus musculu	1409	95	5.6	1052	2	Q7PMV4	Q7pmv4 drosophila
1337	96	5.7	310	2	Q8BB17	Q8be17 vaccinia vl	1410	95	5.6	1270	2	MYPC_MOUSE	Q70468 mus musculu
1338	96	5.7	312	2	Q8BNJ2	Q8bnj2 rabbitipox v	1411	95	5.6	1304	2	Q9VB55	Q9vbe5 drosophila
1339	96	5.7	360	2	Q8N732	Q8n732 homo sapien	1412	95	5.6	1375	2	Q8BV57	Q8bv57 mus musculu
1340	96	5.7	395	2	Q61E78	Q61e78 paracitichth	1413	95	5.6	1450	1	MPSP_CHICK	Q8m147 drosophila
1341	96	5.7	407	1	G1C2_VIBCH	Q9klp4 vibrio chol	1414	95	5.6	1501	2	Q7TTI7	Q7tti7 gallus gall
1342	96	5.7	462	2	Q7RTW1	Q7rtw1 homo sapien	1415	95	5.6	1501	2	Q9QM00	Q9qm00 rattus bp.
1343	96	5.7	462	2	Q7OD44	Q7qdd4 anopheles g	1416	95	5.6	1526	2	Q9V6D5	Q9v6d5 drosophila
1344	96	5.7	570	2	Q6GM29	Q6gm29 xenopus lae	1417	95	5.6	1527	2	Q9V2Z4	Q9v2z4 drosophila
1345	96	5.7					1418	95	5.6				

1419	95	5.6	1863	2	064605	064605	rattus norv
1420	95	5.6	1898	2	09E017	09E017	mus musculus
1421	95	5.6	1904	2	064639	064639	mus musculus
1422	95	5.6	1945	2	096681	096681	dtrosophila
1423	95	5.6	22152	1	08Wx17	08Wx17	homo sapien
1424	94.5	5.6	315	1	HEMA VACC	HEMA VACC	vacccia vi
1425	94.5	5.6	330	2	08C2T8	08C2T8	mus musculus
1426	94.5	5.6	341	2	0819K3	0819K3	branchiocto
1427	94.5	5.6	371	2	06DCN5	06DCN5	kenopus lae
1428	94.5	5.6	381	2	09Y4A4	09Y4A4	homo sapien
1429	94.5	5.6	388	2	08NF28	08NF28	homo sapien
1430	94.5	5.6	485	2	AAH70886	AAH70886	rattus no
1431	94.5	5.6	500	2	09X2B7	09X2B7	dtrosophila
1432	94.5	5.6	553	2	08Wx15	08Wx15	homo sapien
1433	94.5	5.6	556	2	IRL1 HUMAN	IRL1 HUMAN	homo sapien
1434	94.5	5.6	570	2	06GLY1	06GLY1	kenopus lae
1435	94.5	5.6	588	1	C166 CHICK	C166 CHICK	gallus gall
1436	94.5	5.6	593	2	06INM5	06INM5	kenopus lae
1437	94.5	5.6	593	2	AAH72253	AAH72253	kenopus 1
1438	94.5	5.6	628	2	09M208	09M208	bos taurus
1439	94.5	5.6	733	2	09Q2M7	09Q2M7	mus musculus
1440	94.5	5.6	755	2	08CCP8	08CCP8	mus musculus
1441	94.5	5.6	822	1	TRKB HUMAN	TRKB HUMAN	homo sapien
1442	94.5	5.6	822	2	AAK92490	AAK92490	homo sapi
1443	94.5	5.6	838	2	08Wx17	08Wx17	homo sapien
1444	94.5	5.6	868	2	086VR2	086VR2	homo sapien
1445	94.5	5.6	879	2	06PE80	06PE80	mus musculus
1446	94.5	5.6	879	2	AAH58230	AAH58230	mus muscu
1447	94.5	5.6	888	2	UFO MOUSE	UFO MOUSE	mus musculus
1448	94.5	5.6	888	2	080Y03	080Y03	mus musculus
1449	94.5	5.6	891	2	090Y74	090Y74	mus musculus
1450	94.5	5.6	931	2	080747	080747	mus musculus
1451	94.5	5.6	930	2	08CD16	08CD16	mus musculus
1452	94.5	5.6	999	1	MERK HUMAN	MERK HUMAN	homo sapien
1453	94.5	5.6	1083	2	076698	076698	caenorhabd
1454	94.5	5.6	1256	2	035158	035158	rattus norv
1455	94.5	5.6	1327	2	080HL3	080HL3	gallus gall
1456	94	5.6	252	2	086P85	086P85	dtrosophila
1457	94	5.6	275	2	07PVN4	07PVN4	anopheles g
1458	94	5.6	278	2	09QYL3	09QYL3	mus musculus
1459	94	5.6	294	2	08BH36	08BH36	mesocricetu
1460	94	5.6	313	1	HEMA VARV	HEMA VARV	variola vir
1461	94	5.6	313	2	035531	035531	rattus norv
1462	94	5.6	313	2	08AYW3	08AYW3	variola vir
1463	94	5.6	313	2	08BE14	08BE14	variola vir
1464	94	5.6	343	2	06U7R4	06U7R4	mus musculus
1465	94	5.6	343	2	AAK23483	AAK23483	mus muscu
1466	94	5.6	362	2	08CIC7	08CIC7	mus musculus
1467	94	5.6	377	2	080V04	080V04	mus musculus
1468	94	5.6	398	2	07Z3B9	07Z3B9	homo sapien
1469	94	5.6	419	2	086M56	086M56	dtrosophila
1470	94	5.6	484	2	099J08	099J08	mus musculus
1471	94	5.6	508	2	08BJA5	08BJA5	mus musculus
1472	94	5.6	536	2	08BJE2	08BJE2	mus musculus
1473	94	5.6	583	2	022889	022889	arabidopsis
1474	94	5.6	583	2	08VZK7	08VZK7	arabidopsis
1475	94	5.6	602	2	09VFD9	09VFD9	arabidopsis
1476	94	5.6	602	2	AAFS5121	AAFS5121	dtrosophila
1477	94	5.6	821	2	08BF70	08BF70	m mus muscu
1478	94	5.6	883	2	08TTT9	08TTT9	methanobarc
1479	94	5.6	887	2	08YWT7	08YWT7	anabaena sp
1480	94	5.6	943	1	030320	030320	archaeoglob
1481	94	5.6	1010	1	CONT CHICK	CONT CHICK	gallus gall
1482	94	5.6	1280	1	09EPX2	09EPX2	mus musculus
1483	94	5.6	1325	1	YDER_ECOLI	YDER_ECOLI	escherichia
1484	94	5.6	1343	1	VGR2 RAT	VGR2 RAT	rattus norv
1485	94	5.6	1406	2	09GPB7	09GPB7	dtrosophila
1486	94	5.6	1463	2	09V008	09V008	dtrosophila
1487	94	5.6	1945	2	09V491	09V491	dtrosophila
1488	93.5	5.5	259	2	08UVAS	08UVAS	brachydanio
1489	93.5	5.5	261	2	08AU04	08AU04	brachydanio
1490	93.5	5.5	296	2	042404	042404	gallus gall
1491	93.5	5.5	313	2	08UV33	08UV33	brachydanio

1492	93.5	5.5	315	2	06UN41	06UN41	cowpox viru
1493	93.5	5.5	315	2	AAQ73184	AAQ73184	cowpox vi
1494	93.5	5.5	315	2	AAQ73183	AAQ73183	cowpox vi
1495	93.5	5.5	326	2	08UV70	08UV70	brachydanio
1496	93.5	5.5	329	1	CD86 HUMAN	CD86 HUMAN	homo sapien
1497	93.5	5.5	329	2	AAH40261	AAH40261	homo sapi
1498	93.5	5.5	379	2	09CWM1	09CWM1	mus musculus
1499	93.5	5.5	388	2	08R464	08R464	mus musculus
1500	93.5	5.5	392	2	0923L4	0923L4	mus musculus

ALIGNMENTS

RESULT 1

06UX14 PRELIMINARY; PRT; 321 AA.

AC 06UX14; DT 05-JUL-2004 (TrEMBLrel. 27, Created) DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) DE STIGMA. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. NCBI_TaxID=9606; RN [1]

SEQUENCE FROM N.A. RP MEDLINE=2887296; PubMed=12975309; RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.B., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J., Seshagiri S., Simmon L., Singh V., Smith V., Stinson J., Vagstad A., Vandlen R., Watanabe C., Wiand D., Woods K., Xie M.H., Yarusla D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.; RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."; RL Genome Res. 13:2265-2270(2003).

EMBL: AY58341; AA08707.1; -. DR InterPro: IPR003599; IG. DR InterPro: IPR007110; IG-11ke. DR InterPro: IPR003598; IG-C2. DR InterPro: IPR003596; IG-V. DR Pfam: PR00047; IG_2. DR SMART: SM00409; IG_2. DR SMART: SM00408; IG_2; 1. DR SMART: SM00406; IG_1. DR PROSITE: PSS0835; IG LIKE; 2. SQ SEQUENCE 321 AA; 35544 MW; B2AB2B315D39C6E CRC64;

Query Match 100.0%; Score 1688; DB 2; Length 321; Best Local Similarity 100.0%; Pred. No. 1.3e-125; Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLGLHGLTVTPYGRPILEVPESTVTPGPKGVDNLPCTYDPIQGYTVQVVKMLVOR 60
1 MGILLGLLGLHGLTVTPYGRPILEVPESTVTPGPKGVDNLPCTYDPIQGYTVQVVKMLVOR 60
DB 1 MGILLGLLGLHGLTVTPYGRPILEVPESTVTPGPKGVDNLPCTYDPIQGYTVQVVKMLVOR 60

QY 61 GSDPVITFLRDSGSDHIQQAQYQGRLLVSHKVGSDVSLQSTLEMDRSHYTCVWTQTP 120
61 GSDPVITFLRDSGSDHIQQAQYQGRLLVSHKVGSDVSLQSTLEMDRSHYTCVWTQTP 120
DB 61 GSDPVITFLRDSGSDHIQQAQYQGRLLVSHKVGSDVSLQSTLEMDRSHYTCVWTQTP 120

QY 121 DGNQVVRDKTTERVQKLSKRPVTTGSGYGTTVQGMPISTOCARSGSPISYVWYKQ 180
121 DGNQVVRDKTTERVQKLSKRPVTTGSGYGTTVQGMPISTOCARSGSPISYVWYKQ 180
DB 121 DGNQVVRDKTTERVQKLSKRPVTTGSGYGTTVQGMPISTOCARSGSPISYVWYKQ 180

QY 181 QTNNOEPKIVATSTLLFKPAVIVADSGSYCTAKGQVGSFQSHDVIYKFFVVKDSKLKTK 240
181 QTNNOEPKIVATSTLLFKPAVIVADSGSYCTAKGQVGSFQSHDVIYKFFVVKDSKLKTK 240

Db 181 QTNNOBPIKVALISTLLFKPAVIADSGSYCTAKGVSGSEHSDIVKFWKSSKLLKTK 240
 QY 241 TEAPTMTYPLKATSTYKOSMDWTMDGVLGETSAGPGKSLPFAIILLISLCMVVFT 300
 Db 241 TEAPTMTYPLKATSTYKOSMDWTMDGVLGETSAGPGKSLPFAIILLISLCMVVFT 300
 QY 301 MAYIMLCRKTSQOEHYEAR 321
 Db 301 MAYIMLCRKTSQOEHYEAR 321

RESULT 2

AA088707 PRELIMINARY; PRT; 321 AA.
 ID AA088707; AA088707;
 DT 02-MAR-2004 (TReMBLrel. 27, Created)
 DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
 DE STIGMA.
 GN UNQ317.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12975309;
 RA Clark H.F., Gunney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
 Raton D., Foster J., Grimaldi C., Gu Q., Hase P.B., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshgiri S., Simmons L., Singh J., Smith V., Stinson J., Vagstad A.,
 RA Vandlen R., Watanabe C., Wiand D., Woods K., Xie M.H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.,
 RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
 RT Bioinformatics Assessment."
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; AY358341; AA088707.1; -.
 SQ SEQUENCE 321 AA; 35544 MW; B2AB2E3151D39C6E CRC64;

Query Match 100.0%; Score 1688; DB 2; Length 321;
 Best Local Similarity 100.0%; Pred. No. 1,3e-125;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLHLYVDYGRPILEVPEBSVTGPKGDVNLPCYDPLQGYTVLVKMLVOR 60
 Db 1 MGILLGLLLGLHLYVDYGRPILEVPEBSVTGPKGDVNLPCYDPLQGYTVLVKMLVOR 60
 QY 61 GSDPVTITFLRDSGGDHIOQAKYQGRHLVSHKVPDVSLOLSTLEMDRSHYTCETVWTQTP 120
 Db 61 GSDPVTITFLRDSGGDHIOQAKYQGRHLVSHKVPDVSLOLSTLEMDRSHYTCETVWTQTP 120
 QY 121 DGNQVVRDKITELRVOQLSVSKPTVTGSGYGFVTPQGRISLQCARSGSPISYIWKQ 180
 Db 121 DGNQVVRDKITELRVOQLSVSKPTVTGSGYGFVTPQGRISLQCARSGSPISYIWKQ 180
 QY 121 DGNQVVRDKITELRVOQLSVSKPTVTGSGYGFVTPQGRISLQCARSGSPISYIWKQ 180
 Db 121 DGNQVVRDKITELRVOQLSVSKPTVTGSGYGFVTPQGRISLQCARSGSPISYIWKQ 180
 QY 181 QTNNOBPIKVALISTLLFKPAVIADSGSYCTAKGVSGSEHSDIVKFWKSSKLLKTK 240
 Db 181 QTNNOBPIKVALISTLLFKPAVIADSGSYCTAKGVSGSEHSDIVKFWKSSKLLKTK 240
 QY 241 TEAPTMTYPLKATSTYKOSMDWTMDGVLGETSAGPGKSLPFAIILLISLCMVVFT 300
 Db 241 TEAPTMTYPLKATSTYKOSMDWTMDGVLGETSAGPGKSLPFAIILLISLCMVVFT 300
 QY 301 MAYIMLCRKTSQOEHYEAR 321
 Db 301 MAYIMLCRKTSQOEHYEAR 321

RESULT 3

Q9Y279 PRELIMINARY; PRT; 399 AA.
 ID Q9Y279; Q9Y279;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Z391g protein precursor (Ig superfamily protein).
 GN Name=Z391g; Synonyms=Z391G;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20461865; PubMed=11004523;
 RA Iargnaese K., Colieux L., Kloos D.U., Fontes M., Wieacker P.;
 RT "Cloning of Z391g, a novel gene with immunoglobulin-like domains
 RT located on human chromosome X.";
 RL Biochim. Biophys. Acta 1492:522-525(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain;
 MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stempelson M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ushed T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
 RA Krzywinski M.I., Skalsoda U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Kiera M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ13502; CAB51536.1; -.
 DR EMBL; BC010525; AAH0525.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 KW Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 399 Z391g protein.
 SQ SEQUENCE 399 AA; 43987 MW; 735CA3BC58185035 CRC64;

Query Match 100.0%; Score 1688; DB 2; Length 399;
 Best Local Similarity 100.0%; Pred. No. 1,7e-125;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLHLYVDYGRPILEVPEBSVTGPKGDVNLPCYDPLQGYTVLVKMLVOR 60
 Db 1 MGILLGLLLGLHLYVDYGRPILEVPEBSVTGPKGDVNLPCYDPLQGYTVLVKMLVOR 60
 QY 61 GSDPVTITFLRDSGGDHIOQAKYQGRHLVSHKVPDVSLOLSTLEMDRSHYTCETVWTQTP 120
 Db 61 GSDPVTITFLRDSGGDHIOQAKYQGRHLVSHKVPDVSLOLSTLEMDRSHYTCETVWTQTP 120
 QY 121 DGNQVVRDKITELRVOQLSVSKPTVTGSGYGFVTPQGRISLQCARSGSPISYIWKQ 180

```

Dd 121 DGNQVVDKITELEKSVKSPKPTVTTGSGYGFVPOQMRISLCCQARGSPPISYIWKQ 180
Qy 181 QTNNOEPKXVATLSTLLFKPAVIADSGSYFCTAGQVSGEBSHDIYKRVVNDSSKLKTK 240
Dd 181 QTNNOEPKXVATLSTLLFKPAVIADSGSYFCTAGQVSGEBSHDIYKRVVNDSSKLKTK 240
Qy 241 TEAPTTMTYPLKATSTYKQSWMDTMDGYLGSTAGPGKSLPVFAILLISLCMVFT 300
Dd 241 TEAPTTMTYPLKATSTYKQSWMDTMDGYLGSTAGPGKSLPVFAILLISLCMVFT 300
Qy 301 MAYIMLCRKTSQOEHYVEAR 321
Dd 301 MAYIMLCRKTSQOEHYVEAR 321

RESULT 4
Q80WA3 PRELIMINARY; PRT; 280 AA.
AC Q80WA3;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein BC025105.
GN Name=BC025105;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uebin T.B., Tomilyski S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skelton U., Smallie D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025105; AAH25105.1;
DR MGD; MGI:2679720; BC025105.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Hypothetical protein.
SQ SSOURCE 280 AA; 31467 MW; 3F099AEE96CE8977 CRC64;

Query Match 43.1%; Score 728; DB 2; Length 280;
Best Local Similarity 47.0%; Pred. No. 1.5e-49;
Matches 151; Conservative 29; Mismatches 45; Indels 96; Gaps 2;
Qy 1 MGILLGLLGLTVDVYGRPILEVPESVTPGPKGVNLPCTYDPLQGYTVLVKMLVOR 60
Dd 1 MEIISGGLFLGHLIVLVYGHPTLTKTPESVTPGPKGVNLPCTYDPLQGYTVLVKMLVOR 60

```

```

Qy 61 GSDPVITFLRSDSSGDHIOAQKYGRLVHSHKVPDVSLOLSTLEMDRSHYTCVNTQTP 120
Dd 61 GSDSVTLFLRSDSSGDHIOAQKYGRLVHSHKVPDVSLOLSTLEMDRSHYTCVNTQTP 120
Qy 121 DGNQVVDKITELEKSVKSPKPTVTTGSGYGFVPOQMRISLCCQARGSPPISYIWKQ 180
Dd 121 DGNQVVDKITELEKSVKSPKPTVTTGSGYGFVPOQMRISLCCQARGSPPISYIWKQ 180
Qy 121 DGNQVVDKITELEKSVKSPKPTVTTGSGYGFVPOQMRISLCCQARGSPPISYIWKQ 180
Dd 121 DGNQVVDKITELEKSVKSPKPTVTTGSGYGFVPOQMRISLCCQARGSPPISYIWKQ 180
Qy 181 QTNNOEPKXVATLSTLLFKPAVIADSGSYFCTAGQVSGEBSHDIYKRVVNDSSKLKTK 240
Dd 181 QTNNOEPKXVATLSTLLFKPAVIADSGSYFCTAGQVSGEBSHDIYKRVVNDSSKLKTK 240
Qy 142 -----RIN 144
Dd 142 -----RIN 144
Qy 241 TEAPTTMTYPLKATSTYKQSWMDTMDGYLGSTAGPGKSLPVFAILLISLCMVFT 300
Dd 241 TEAPTTMTYPLKATSTYKQSWMDTMDGYLGSTAGPGKSLPVFAILLISLCMVFT 300
Qy 145 TEAPTTMTYPLKATSTYKQSWMDTMDGYLGSTAGPGKSLPVFAILLISLCMVFT 204
Dd 145 TEAPTTMTYPLKATSTYKQSWMDTMDGYLGSTAGPGKSLPVFAILLISLCMVFT 204
Qy 301 MAYIMLCRKTSQOEHYVEAR 321
Dd 301 MAYIMLCRKTSQOEHYVEAR 321
Qy 205 IPYILFRCTFOOEYVYGVSR 225
Dd 205 IPYILFRCTFOOEYVYGVSR 225

RESULT 5
BAC30780 PRELIMINARY; PRT; 280 AA.
AC BAC30780;
DT 14-APR-2004 (Tremblrel. 27, Created)
DT 14-APR-2004 (Tremblrel. 27, Last sequence update)
DT 14-APR-2004 (Tremblrel. 27, Last annotation update)
DE Adult male aorta and vein cDNA, RIKEN full-length enriched library,
DE clone:A53061A1 product:hypothetical immunoglobulin and major
DE histocompatibility complex domain/immunoglobulin subtype containing
DE protein, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

```

RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hazada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yonekura Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Arteria and vein;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasubawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akanita S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK041014; BAC30780.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 280 AA; 31467 MW; 3F039A8B96CE8977 CRC64;
 QY Query Match 43.1%; Score 728; DB 2; Length 280;
 Best Local Similarity 47.0%; Pred. No. 1.5e-49;
 Matches 151; Conservative 29; Mismatches 45; Indels 96; Gaps 2;
 DB 1 MGILLGLGHTLVTPYGRPIEVEPSVTPKSGDVNLPCTYDPLQGYQVTVKVLNR 60
 1 MEIISGSLFLGHLIVLTPYGRPIEVEPSVTPKSGDVNLPCTYDPLQGYQVTVKVLNR 60
 QY 61 GSDPVTIFLSDSGSDHIOQAKYQGRLVSHKVPDVSLOSTLEMDRSHYTCETWQTP 120
 61 GSDSVITFLRDSGSDHIOQAKYQGRLVSHKVPDVSLOSTLEMDRSHYTCETWQTP 120
 DB 61 GSDSVITFLRDSGSDHIOQAKYQGRLVSHKVPDVSLOSTLEMDRSHYTCETWQTP 120
 QY 121 DGNQVVRDKITELRVQGLSVSKPTVTGSGYFTVQGMKISLQCCARSGSPISYIYWKQ 180
 121 DGNQVVRDKITELRVQGLSVSKPTVTGSGYFTVQGMKISLQCCARSGSPISYIYWKQ 180
 DB 121 DGNQVVRDKITELRVQGLSVSKPTVTGSGYFTVQGMKISLQCCARSGSPISYIYWKQ 180
 QY 181 QTNNOPIKAVATSTLLFKRAVLADSGSYCTAKGQVSGHSDIYKFAVKDSKLLKTK 240
 181 QTNNOPIKAVATSTLLFKRAVLADSGSYCTAKGQVSGHSDIYKFAVKDSKLLKTK 240
 DB 142 -----RIN 144
 QY 241 TEAPTTMYPLKATSTVYKQSGMDWTMDGYLGETSAGPKSLPVFAIIILISLCMVFT 300
 241 TEAPTTMYPLKATSTVYKQSGMDWTMDGYLGETSAGPKSLPVFAIIILISLCMVFT 300
 DB 145 TEAPTTMHSLEATITMSSTSDITNGTGTLETTINGSGNLPFALIPITISLCIVAVT 204
 145 TEAPTTMHSLEATITMSSTSDITNGTGTLETTINGSGNLPFALIPITISLCIVAVT 204
 QY 301 MAYIMLCRKTSQGEHYEAR 321
 301 MAYIMLCRKTSQGEHYEAR 321
 DB 205 IPIILFRCRFPQOEYVGVSR 225
 205 IPIILFRCRFPQOEYVGVSR 225
 RESULT 6
 JAM1_HUMAN STANDARD; PRT; 299 AA.
 AC O9Y624;
 ID JAM1_HUMAN
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion
 DE molecule 1) (PAM-1) (Platelet FII receptor) (UMQ264/PRO301).
 GN Name=JAM1; Synonyms=JAM1, JCM1;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=99323940; PubMed=10395639;
 RA Ozaki H., Ishii K., Horinouchi H., Arai H., Kawamoto T., Okawa K.,
 RA Iwanami A., Kita T.,
 RT "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
 RT of junctional adhesion molecule in human endothelial cells.",
 RL J. Immunol. 163:553-557(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.,
 RA Kornecak E.,
 RT "Molecular cloning and sequencing of the cDNA of FII receptor, a novel
 RT Ig superfamily member from human platelets.",
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Naik U.P., Naik M.U., Deleon P., Spychala J.,
 RT "Cloning and characterization of PAM-1, a novel platelet adhesion
 RT molecule involved in platelet activation.",
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
 RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
 RA Ansoerg W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
 RA Mewes H.-W., Oettermann B., Obermaier B., Tampe J., Heubner D.,
 RA Wambutt R., Korn B., Klein M., Poustka A.,
 RT "Towards a catalog of human genes and proteins: sequencing and
 RT analysis of 500 novel complete protein coding human cDNAs.",
 RL Genome Res. 11:422-435(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887286; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gunney A.L., Absaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Choi C., Crowley C., Currell B., Devel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Sehnagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yamanura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.,
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.",
 RL Genome Res. 13:2265-2270(2003).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.T., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Guttmann J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywicki M.I., Skalska U., Smallog D.E.,
 RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 28-42.

RA Zhang Z., Henzel W. ;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites." ;
 RL Submitted (JUN-2004) to Swiss-Prot.
 CC -1- FUNCTION: Seems to plays a role in epithelial tight junction
 CC formation. Appears early in primordial forms of cell junctions and
 CC recruits PARD3. The association of the PARD6-PARD3 complex may
 CC prevent the interaction of PARD3 with JAM1, thereby preventing
 CC tight junction assembly (By similarity). Plays a role in
 CC regulating monocyte transmigration involved in integrity of
 CC epithelial barrier. Involved in platelet activation.
 CC -1- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
 CC association between PARD3 and PARD6 probably disrupts this
 CC interaction (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Localized at tight junctions of both
 CC epithelial and endothelial cells.
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).

DR EMBL, AF11713; AAD2050.1; -
 DR EMBL, AF207907; AAF22829.1; -
 DR EMBL, AF172398; AAD48877.1; -
 DR EMBL, AL136649; CAB66584.1; -
 DR EMBL, AY358896; AAQ89255.1; -
 DR EMBL, BC001533; AAH01533.1; -
 DR PIR, A59406; S56749.
 DR PDB, INBO: X-ray; A/B=25-233.
 DR Genew, HGNC:14685; F1LR.
 DR MIM, 605721; -
 DR GO, GO:0005911; C:intracellular function; TAS.
 DR GO, GO:0006954; P:inflammatory response; TAS.
 DR InterPro, IPR007110; Ig-like.
 DR Pfam, PF00047; Ig_2.
 DR PROSITE, PSS0835; IG_LIKE_2.
 KW 3D-structure; Direct protein sequencing; Glycoprotein;
 KW Immunoglobulin domain; Repeat; Signal; Tight junction; Transmembrane.
 FT CHAIN 1 27 Junctional adhesion molecule 1.
 FT DOMAIN 28 238 Extracellular (Potential).
 FT TRANSMEM 239 259 Potential.
 FT DOMAIN 260 299 Cytoplasmic (Potential).
 FT DOMAIN 28 125 Ig-like V-type 1.
 FT DISULFID 135 228 Ig-like V-type 2.
 FT DISULFID 50 109 Potential.
 FT DISULFID 153 212 Potential.
 FT CARBOHYD 185 185 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match 10.6%; Score 178.5; DB 1; Length 299;
 Best Local Similarity 26.5%; Pred. No. 6.6e-06;
 Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLGLHTVDTYGRPILEVPSVTGPMKGDVNLPTCTYDPLQGYQVLYKVLVOR 60
 DB 17 LAILLGLSLAGSVTVHS-SEPEVRIPEN-----NPKVLSCAV---SGFSSPREVM--- 62
 QY 61 GSDPVTIFLRDSSGDHIOAKYQGRHLVSHK-----VPGDVSILSTLMDRSHYTCFV 115
 DB 63 -----KFDGDTTRLVLCYNKKITASJEDRTVLPPTGTRFSVTRR--DTGTYTCMV 111
 QY 116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTSGGYGFTVPGQMRISLQCOAR-GSPDIS 174
 DB 112 SEEGGNSYGEVKKVLYL-----VPSKPTVNIPS-----SATIGNRAVLTCSEDDGSPSE 163

QY 175 YIYWK-----QQTN-----NOEPIKVAITLSTLLPKPAVIADSGSYFCTAKGVSEQH 222
 DB 164 YTFWKGQIVMPTPKSTRFSSNSYVNLPTTGELVFDPLASDGTGEYSCEARNGYGTPT 223
 QY 223 SDIVK 227
 DB 224 SNAVR 228

RESULT 7
 AAG28379 PRELIMINARY; PRT; 299 AA.
 ID AAG28379
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE Full receptor protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20537956; Pubmed=11087121;
 RA Gupta S.K., Pillarisetti K., Ohlstein B.H.;
 RT "Platelet agonist P1 receptor is a member of the immunoglobulin
 RT superfamily and identical with junctional adhesion molecule (JAM).
 RT regulation of expression in human endothelial cells and macrophages." ;
 RL IUBMB Life 50:51-56(2000).
 DR EMBL, AF191495; AAG28379.1; -
 KW Receptor.
 SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match 10.6%; Score 178.5; DB 2; Length 299;
 Best Local Similarity 26.5%; Pred. No. 6.6e-06;
 Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLGLHTVDTYGRPILEVPSVTGPMKGDVNLPTCTYDPLQGYQVLYKVLVOR 60
 DB 17 LAILLGLSLAGSVTVHS-SEPEVRIPEN-----NPKVLSCAV---SGFSSPREVM--- 62
 QY 61 GSDPVTIFLRDSSGDHIOAKYQGRHLVSHK-----VPGDVSILSTLMDRSHYTCFV 115
 DB 63 -----KFDGDTTRLVLCYNKKITASJEDRTVLPPTGTRFSVTRR--DTGTYTCMV 111
 QY 116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTSGGYGFTVPGQMRISLQCOAR-GSPDIS 174
 DB 112 SEEGGNSYGEVKKVLYL-----VPSKPTVNIPS-----SATIGNRAVLTCSEDDGSPSE 163
 QY 175 YIYWK-----QQTN-----NOEPIKVAITLSTLLPKPAVIADSGSYFCTAKGVSEQH 222
 DB 164 YTFWKGQIVMPTPKSTRFSSNSYVNLPTTGELVFDPLASDGTGEYSCEARNGYGTPT 223
 QY 223 SDIVK 227
 DB 224 SNAVR 228

RESULT 8
 BAC11436 PRELIMINARY; PRT; 299 AA.
 ID BAC11436
 AC BAC11436
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE cDNA Flj30671 file, clone PLACE1005544, moderately similar to Mus
 DE musculus junctional adhesion molecule (Jam) mRNA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

```

RC TISSUE=placenta;
RA Isegai T., Oca T., Nishikawa T., Hayaashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hito Y., Saito K.,
RA Yamamoto J., Nakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuo Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nishimura K.,
RT "NEBO human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075152; BAC11436.1; -.
SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match 10.6%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 6.6e-06;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLGLHGLTVDTYGRPILEVPSVTGPKGVDNLPCTYDPLQGYQVLVKKLVQR 60
DB 17 LAILLCSLALGSYTVHS-SEPEVRIPEN-----NPKLSGCAV---SGFSSPREVW---- 62
QY 61 GSDPVTITFLDSSGDHIQQAQYQGRLLVSHK-----VPGDVSQQLSTLEMDRSHYTCV 115
DB 63 -----KFDGDTTRLVLCVNNKKTASIEDRVTFPLTGITRKSVTRE--DGTITCMV 111
QY 116 TWQTPGNOVVRDKITELRVQKLSVSKPTVTGSGYGVTVPGQWRISLQCAR-GSPPIIS 174
DB 112 SEEGGNSYGEVKKVLIIVL---VPPSKPTVNIPS---SATIGNRAVLTCSEQDGSPSE 163
QY 175 YIMYK-----QQTN-----NOEPIKVALTLTLFPRKPAVINDSSGYFCTAKQVSEQH 222
DB 164 YIMFKGIVMPITPKSTRAFSSSYVLPNTGELVDPDLSASDTGEVSCBARNGYGT 223
QY 223 SDIVK 227
DB 224 SNAVR 228

RESULT 9
AA084556 PRELIMINARY; PRT; 299 AA.
AC AA084556;
DT 02-MAR-2004 (TREMURel. 27, Created)
DT 02-MAR-2004 (TREMURel. 27, Last sequence update)
DT 02-MAR-2004 (TREMURel. 27, Last annotation update)
DE JAM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RA Wenzel K., Felix S.B., Flachmeier C., Heere P., Schulze W.,
RA Grunewald I., Pankow H., Hewelt A., Scherneck S., Bauer D.,
RA Hoehe M.R.,
RT "Identification and Characterization of KAT, a Novel Gene
RT Preferentially Expressed in Several Human Cancer Cell Lines."
RL Biol. Chem. 384:763-775(2003).
DR EMBL; AF490407; AA084556.1; -.
SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match 10.6%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 6.6e-06;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLGLHGLTVDTYGRPILEVPSVTGPKGVDNLPCTYDPLQGYQVLVKKLVQR 60
DB 17 LAILLCSLALGSYTVHS-SEPEVRIPEN-----NPKLSGCAV---SGFSSPREVW---- 62
QY 61 GSDPVTITFLDSSGDHIQQAQYQGRLLVSHK-----VPGDVSQQLSTLEMDRSHYTCV 115
DB 63 -----KFDGDTTRLVLCVNNKKTASIEDRVTFPLTGITRKSVTRE--DGTITCMV 111
QY 116 TWQTPGNOVVRDKITELRVQKLSVSKPTVTGSGYGVTVPGQWRISLQCAR-GSPPIIS 174
DB 112 SEEGGNSYGEVKKVLIIVL---VPPSKPTVNIPS---SATIGNRAVLTCSEQDGSPSE 163

```

```

DB 112 SEEGGNSYGEVKKVLIIVL---VPPSKPTVNIPS---SATIGNRAVLTCSEQDGSPSE 163
QY 175 YIMYK-----QQTN-----NOEPIKVALTLTLFPRKPAVINDSSGYFCTAKQVSEQH 222
DB 164 YIMFKGIVMPITPKSTRAFSSSYVLPNTGELVDPDLSASDTGEVSCBARNGYGT 223
QY 223 SDIVK 227
DB 224 SNAVR 228

RESULT 10
A33 HUMAN
ID A33 HUMAN STANDARD; PRT; 319 AA.
AC 099795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cell surface A33 antigen precursor (Glycoprotein A33).
GN Name=GP33;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Colon carcinoma;
RX MEDLINE=97165045; PubMed=9012807;
RA Heath J.K., White S.J., Johnstone C.N., Catmel B., Simpson R.J.,
RA Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA Scott A.M., Rittler G., Cohen L., Welt S., Old L.J., Nice B.C.,
RA Burgess A.W.;
RT "The human A33 antigen is a transmembrane glycoprotein and a novel
RT member of the immunoglobulin superfamily."
RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
RN 12
RP POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=97396159; PubMed=9245713;
RA Rittler G., Cohen L.S., Nice B.C., Catmel B., Burgess A.W.,
RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA Simpson R.J.;
RT "Characterization of posttranslational modifications of human A33
RT antigen, a novel palmitoylated surface glycoprotein of human
RT gastrointestinal epithelium."
RL Biochem. Biophys. Res. Commun. 236:682-686(1997).
CC 1- FUNCTION: May play a role in cell-cell recognition and signaling.
CC 1- SUBCELLULAR LOCATION: Type I membrane protein.
CC 1- TISSUE SPECIFICITY: Expressed in normal gastrointestinal
CC epithelium and in 95% of colon cancers.
CC 1- PTM: N-glycosylated, contains approximately 8 kDa of N-linked
CC carbohydrate.
CC 1- PTM: Palmitoylated.
CC 1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC 1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL; U79725; AAC0957.1; -.
DR HSSP; 088792; 1F97.
DR Genew; HGNC:4445; GPA33.
DR MIM; 602171; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Antigen; Direct protein sequencing; Glycoprotein;

```


Immunoglobulin domain; Lipoprotein; Palmitate; Signal; Transmembrane.

FT STGNAL 1 21
 FT CHAIN 22 319 Cell surface A33 antigen.
 FT DOMAIN 22 235 Extracellular (Potential).
 FT TRANSMEM 236 256 Potential.
 FT DOMAIN 257 319 Cytoplasmic (Potential).
 FT DOMAIN 22 134 Ig-like V-type.
 FT DOMAIN 140 227 Ig-like C2-type.
 FT DOMAIN 258 261 Poly-Cys.
 FT DISULFID 43 117 Potential.
 FT DISULFID 146 222 Potential.
 FT CARBOHYD 162 211 Potential.
 FT CARBOHYD 112 112 N-linked (GlcNAc...)
 FT CARBOHYD 200 200 N-linked (GlcNAc...)
 FT CARBOHYD 223 223 N-linked (GlcNAc...)
 SQ SEQUENCE 319 AA, 35632 MW, 98PCTAAAF45C2408E CRC64;

Query Match 10.5%; Score 177; DB 1; Length 319;
 Best Local Similarity 27.5%; Pred. No. 9.4e-06;
 Matches 64; Conservative 39; Mismatches 94; Indels 36; Gaps 11;

DY 4 LGLLLGLHVTDTYGRPILEVPESVYGPWG-DVNLPTCTYDPLQGYTVLVKX-LVQR 60
 DB 8 VLMTLCARVTVDAS---VETPODVLASQGSVTLPTCTYHTSTSSREGLIQWDKLLT 64
 QY 61 GSDPYTIFLADSSGDHIQQAQYQGRLVSHKV-PGVLSLSTLMDRSHYTCVYWT 119
 DB 65 HTERVVIW-PFSNKNYHIGELYKNRVSISNNASQSDASITTDQLTWADNGTYESVLS 123
 QY 120 P-DGNQVVRDKITELRYQKLSVKPTWTGSGYFTVPGMRISLQCAR-GSPPISYIW 177
 DB 124 DLGN-----TKSRRLVLVPPSKPEGIGETI-IGNNIQLTQSGKSGSPTPQYSW 175

DY 178 YKQQTNOE-----PIKVAITSTLLFKPAVIADSGSYCTAKGVSE 220
 DB 176 KRYVILNQEQPLAQPASQGVSLKNIST-----DTSGYICTSSNEGQTQ 220

RESULT 11
 AAH69705 PRELIMINARY; PRT; 319 AA.
 AC AAH69705;
 DT 20-MAY-2004 (Tremblrel. 27, Created)
 DT 20-MAY-2004 (Tremblrel. 27, Last sequence update)
 DT 20-MAY-2004 (Tremblrel. 27, Last annotation update)
 DE Transmembrane glycoprotein A33.
 GN GPA33.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_taxonomy:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
 RA Krzywinski M.I., Skala U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12];
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC69705; AAH69705.1; -.
 KW Transmembrane.
 SQ SEQUENCE 319 AA, 35632 MW, 98PCTAAAF45C2408E CRC64;

Query Match 10.5%; Score 177; DB 2; Length 319;
 Best Local Similarity 27.5%; Pred. No. 9.4e-06;
 Matches 64; Conservative 39; Mismatches 94; Indels 36; Gaps 11;

DY 4 LGLLLGLHVTDTYGRPILEVPESVYGPWG-DVNLPTCTYDPLQGYTVLVKX-LVQR 60
 DB 8 VLMTLCARVTVDAS---VETPODVLASQGSVTLPTCTYHTSTSSREGLIQWDKLLT 64
 QY 61 GSDPYTIFLADSSGDHIQQAQYQGRLVSHKV-PGVLSLSTLMDRSHYTCVYWT 119
 DB 65 HTERVVIW-PFSNKNYHIGELYKNRVSISNNASQSDASITTDQLTWADNGTYESVLS 123
 QY 120 P-DGNQVVRDKITELRYQKLSVKPTWTGSGYFTVPGMRISLQCAR-GSPPISYIW 177
 DB 124 DLGN-----TKSRRLVLVPPSKPEGIGETI-IGNNIQLTQSGKSGSPTPQYSW 175

DY 178 YKQQTNOE-----PIKVAITSTLLFKPAVIADSGSYCTAKGVSE 220
 DB 176 KRYVILNQEQPLAQPASQGVSLKNIST-----DTSGYICTSSNEGQTQ 220

RESULT 12
 AAH69723 PRELIMINARY; PRT; 319 AA.
 AC AAH69723;
 DT 20-MAY-2004 (Tremblrel. 27, Created)
 DT 20-MAY-2004 (Tremblrel. 27, Last sequence update)
 DT 20-MAY-2004 (Tremblrel. 27, Last annotation update)
 DE Transmembrane glycoprotein A33.
 GN GPA33.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_taxonomy:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
 RA Krzywinski M.I., Skala U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12];
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX Strausberg R.;

RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC069723; AAH69723.1; -.
 KM Transmembrane.
 SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAR45C2408E CRC64;

Query Match 10.5%; Score 177; DB 2; Length 319;
 Best Local Similarity 27.5%; Pred. No. 9,4e-06;
 Matches 64; Conservative 39; Mismatches 94; Indels 36; Gaps 11;

QY 4 LGLLLGLHLYDTYGRPLLEVPESVTPGPKG-DVNLPCITYDPLQGYTVLVKM--LVQR 60
 DB 8 VMTLCAVAVTVDAIS--VETPODVLRASQGSVTLPCITYHTSTSSRGLIQMDKLLLT 64
 QY 61 GSDPVITFLRDSGDHIQQAQYQGRLVSHKV-PCGVSLQSLTEMDRSHYTCVYWTQ 119
 DB 65 HTRRVYIV-PFSKNVYIHLELYKNRVSISNNAEQSDASTIIDQLTMADNGTECSVLS 123
 QY 120 P-DGNOVVDKITELRVQKLSVSKPVTVTGSGYGFVPGQMRLSLOQAR-GSPPISTY 177
 DB 124 DLKGN-----TKSRVRLVLVPPSKPCGIEGERT-IGNNIQLTCQSGESPTPQYSW 175
 QY 178 YKQQTNNQ-----PIKATLSTLFPKPAVADSGSYFCTAKGVGSE 220
 DB 176 KRYNIINQEQPLAQPASGQPVSLKNIST-----DTSGYITCTSSNEGTQ 220

RESULT 13

AAH69745 PRELIMINARY; PRT; 319 AA.

AC AAH69745; PRELIMINARY; PRT; 319 AA.
 DT 20-MAY-2004 (TrEMBLrel. 27, Created)
 DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
 DT 20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
 DE Transmembrane glycoprotein A33.

OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang U., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smalov D.E., Schmech A., Schein J.E.,
 Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC069745; AAH69745.1; -.
 KM Transmembrane.
 SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAR45C2408E CRC64;

Query Match 10.5%; Score 177; DB 2; Length 319;

Best Local Similarity 27.5%; Pred. No. 9,4e-06;
 Matches 64; Conservative 39; Mismatches 94; Indels 36; Gaps 11;

QY 4 LGLLLGLHLYDTYGRPLLEVPESVTPGPKG-DVNLPCITYDPLQGYTVLVKM--LVQR 60
 DB 8 VMTLCAVAVTVDAIS--VETPODVLRASQGSVTLPCITYHTSTSSRGLIQMDKLLLT 64
 QY 61 GSDPVITFLRDSGDHIQQAQYQGRLVSHKV-PCGVSLQSLTEMDRSHYTCVYWTQ 119
 DB 65 HTRRVYIV-PFSKNVYIHLELYKNRVSISNNAEQSDASTIIDQLTMADNGTECSVLS 123
 QY 120 P-DGNOVVDKITELRVQKLSVSKPVTVTGSGYGFVPGQMRLSLOQAR-GSPPISTY 177
 DB 124 DLKGN-----TKSRVRLVLVPPSKPCGIEGERT-IGNNIQLTCQSGESPTPQYSW 175
 QY 178 YKQQTNNQ-----PIKATLSTLFPKPAVADSGSYFCTAKGVGSE 220
 DB 176 KRYNIINQEQPLAQPASGQPVSLKNIST-----DTSGYITCTSSNEGTQ 220

RESULT 14

AAH69761 PRELIMINARY; PRT; 319 AA.

AC AAH69761; PRELIMINARY; PRT; 319 AA.
 DT 20-MAY-2004 (TrEMBLrel. 27, Created)
 DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
 DT 20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
 DE Transmembrane glycoprotein A33.

OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang U., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smalov D.E., Schmech A., Schein J.E.,
 Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC069761; AAH69761.1; -.
 KM Transmembrane.
 SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAR45C2408E CRC64;

Query Match 10.5%; Score 177; DB 2; Length 319;
 Best Local Similarity 27.5%; Pred. No. 9,4e-06;
 Matches 64; Conservative 39; Mismatches 94; Indels 36; Gaps 11;

QY 4 LGLLLGLHLYDTYGRPLLEVPESVTPGPKG-DVNLPCITYDPLQGYTVLVKM--LVQR 60
 DB 8 VMTLCAVAVTVDAIS--VETPODVLRASQGSVTLPCITYHTSTSSRGLIQMDKLLLT 64


```

Qy      61 GSPPTVPIFLRSDSGDHIOQAQGRHLSHVHKV-PEDVSLTQSLTEMDRSHYTCQVMOQ 119
      65 HTRRVAIV-PFSKNKIYHIGELTKNKRISISNNAQSDASITTDQLMAANGTECEVSILMS 123
Db      120 P-DGNQVVDKDTIELTVOKLSVSKPTVTGSGYGFVEQGRMHSIOCCAR-GSPPISYIW 177
      124 DLEGN-----TKSRVRLIVLPSPKPCGCIEGETI-IGNNIQLTCSKKGSPFPQYSW 175
Qy      178 YKOQTNOQ-----PIKATLSLEFLPRAVIADSGSYFTAKQVSE 220
      176 KRNIINQGEPLAQPSGQPVSLKSIIST-----DTSGYITCTSSNBETQ 220

```

```

Db      124 DLEGN-----TKSNRLVLVPPSSKEPCGIEGTI-IGNNIQLTQOSKXGSGTPLYSN 175
      178 YKQOTNOE-----PIVATLSTLLEKPAVIADSGSYFCTAKQVSE 220
      176 KRYNIINOEPLAQASGAPVSLKRIST-----DTSGYICTSNSEEGTQ 220

Search completed: January 4, 2005, 06:10:20
Job time : 175 secs

```

Search completed: January 4, 2005, 06:10:20
Job time : 175 secs

RESULT 15	ID	AAH69789	PRELIMINARY;	PRT;	319 AA.
AC	AAH69789;				
AD	20-MAY-2004 (TREMBLrel. 27, Created)				
DT	20-MAY-2004 (TREMBLrel. 27, Last sequence update)				
DT	20-MAY-2004 (TREMBLrel. 27, Last annotation update)				
DE	Transmembrane glycoprotein A33.				
GN	GPA33.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID:9606;				
RY	SEQUENCE FROM N.A.				
RC	TISSUE=PCR rescued clones;				
RX	MEDLINE=22388257; PubMed=1477932.				
RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Staubert R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,				
RA	Altshul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Zeehan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Rana S.S., Quellan N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Halyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahney J., Helton E., Kertleman M., Madden A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Maden A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodríguez R.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,				
RA	Krzywnicki M.I., Skalska U., Smallus D.B., Scherch A., Schein J.E.,				
RA	Jones S.J., Marx M.A.				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=PCR rescued clones;				
RA	Strauberg R.;				
RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: BC0659789; AAH69789.1; --				
KM	Transmembrane				
SC	SEQUENCE 319 AA; 35632 MW; 98EC7AFA5C2408E ⁵ CRC64;				
Query Match	10.5%; Score 177; DB 2; Length 319;				
Best Local Similarity	27.5%; Pred. No. 9.4e-06;				
Matches	64; Conservative 39; Mismatches 94; Indels 36; Gaps 11.				
QY	4 ILGLLLGLHYDVTYGRILEYPRPSVYTPKMG-DVNLCTYDPLQGYQLVYK--LYQR 60				
DB	8 VLWLTICAVRIVTDAIS---VETPPOVLRLASQGSYTLCTYHTSTSSREGILQWKLIT 64				
QY	61 GSDPTTILRLSSGCDHIQQAQYQGRILAHYSHKV-PGDVSLQLSTLEMDRSHYTCVWT 119				
DB	65 HTERVIVL-PRSNKRYIHGELYKRVISVSNNAEGSDAISTIDQLTMAIDNGTREGCVSLMS 123				
QY	120 P-DGNQVVRDKITELRVQKLSVSKRTVTGSGYGTFTPOGKRISLQCOAR-GSPISIV 177				

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 06:06:41 ; Search time 27 Seconds
(without alignments)
1143.910 Million cell updates/sec

Title: US-10-767-374-2
Perfect score: 1688
Sequence: 1 MGILLGLLGLHITVDYGR.....ATYMLCKRTSQGHVYEAAR 321

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR 79:.*
1: d1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	178.5	10.6	299	2	S56749
2	172	10.2	7962	2	I38346
3	169	10.0	365	2	JC7780
4	143.5	8.5	1052	2	B49120
5	139.5	8.3	3707	2	S18252
6	138.5	8.2	1323	2	PN0568
7	138.5	8.2	4162	2	T42633
8	136	8.1	584	2	T08678
9	133.5	7.9	5175	2	T20992
10	133.5	7.9	5198	2	T43290
11	133	7.9	1106	1	PFHUGB
12	132.5	7.8	765	2	C42632
13	132.5	7.8	812	2	B42632
14	132.5	7.8	932	2	A42632
15	132.5	7.8	1272	2	S26180
16	132	7.8	1896	2	T08851
17	131	7.8	4391	2	A38096
18	129.5	7.7	1040	2	A34685
19	129.5	7.7	3375	2	T19821
20	129	7.6	1427	2	I51669
21	128.5	7.6	338	2	JC5519
22	127.5	7.6	1906	1	S68235
23	125.5	7.4	1259	2	A43425
24	125	7.4	351	2	JH0396
25	124	7.3	833	1	IJB0NC
26	124	7.3	1344	2	T14316
27	123.5	7.3	458	1	MMMSR1
28	123.5	7.3	521	2	JC1508
29	123.5	7.3	1091	1	IJCNTL

30	122.5	7.3	761	1	IJTHNG	neural cell adhest
31	122.5	7.3	1258	1	A39540	neural cell adhest
32	120.5	7.1	458	2	JC1509	biliary glycoprote
33	120.5	7.1	538	2	JC2457	vascular cell adhe
34	120	7.1	1033	2	S19247	cell adhesion prot
35	119.5	7.1	1036	2	S22383	axonal precursor
36	119.5	7.1	417	2	JH0394	biliary glycoprote
37	119.5	7.1	464	2	C30127	transmembrane carc
38	119.5	7.1	483	2	T17346	hypothetical prote
39	119.5	7.1	526	1	A32164	biliary glycoprote
40	119.5	7.1	725	1	IJMSNG	neural cell adhest
41	119.5	7.1	725	2	JE0100	neural cell adhest
42	119.5	7.1	1115	1	IJMSNL	neural cell adhest
43	119	7.0	457	1	HLMSP3	poliovirus recepto
44	119	7.0	1091	2	A58532	glial cell membran
45	119	7.0	26926	1	I38344	titin, cardiac mus
46	118.5	7.0	333	2	A31923	amalgam protein pr
47	118.5	7.0	458	2	S68177	C-CAM2a protein is
48	118.5	7.0	458	2	S23969	cell-adhesion mole
49	118.5	7.0	539	2	A44783	ecto-ATPase precu
50	118.5	7.0	816	2	A49151	fibroblast growth
51	118.5	7.0	1011	2	T13669	neuromusculin - fr
52	118.5	7.0	1694	2	S50065	intercellular adhe
53	118	7.0	547	1	S28904	protein-tyrosine k
54	118	7.0	1338	2	S09982	limbic-system-asso
55	117.5	7.0	338	2	JC4776	non-specific cross-
56	117.5	7.0	344	2	A27681	neural cell adhest
57	117.5	7.0	1092	1	JN0635	neuroglial - fruit
58	117.5	7.0	1239	1	A32579	vascular cell adhe
59	117	6.9	739	2	J80675	neural cell adhest
60	117	6.9	858	1	IJRNMC	tumor suppressor p
61	117	6.9	1447	2	A54100	protein-tyrosine k
62	116.5	6.9	806	2	A35863	transient axonal g
63	116.5	6.9	1040	2	A49356	kinase-like protei
64	116.5	6.9	1051	2	A39712	neurotrophin - rat
65	116	6.9	344	2	I56551	proteoglycan - fru
66	116	6.9	6658	2	T13931	T-cell receptor de
67	115.5	6.8	292	2	S03421	gene B7-2 protein
68	115.5	6.8	293	2	A40131	neural cell adhest
69	115.5	6.8	309	2	I49522	platelet-endothel
70	115.5	6.8	725	2	JE0099	neural cell adhest
71	115.5	6.8	728	2	A40096	probable neural ce
72	115.5	6.8	1257	1	A41060	PRR2 alpha - human
73	115	6.8	1209	2	T42718	biliary glycoprote
74	114.5	6.8	478	2	I53960	PRR2 delta - human
75	114.5	6.8	521	2	S34338	neural cell adhest
76	114.5	6.8	538	2	I68093	hypothetical prote
77	114.5	6.8	1088	1	IJXJNL	intercellular adhe
78	114.5	6.8	1173	2	T25893	poliovirus recepto
79	114	6.8	544	2	JC5018	neural cell adhest
80	113.5	6.7	530	2	A53437	cell adhesion mole
81	113	6.7	1277	2	T30532	cell adhesion mole
82	112.5	6.7	321	2	JH0395	cell adhesion mole
83	112.5	6.7	345	2	JC4025	cell adhesion mole
84	112.5	6.7	1259	2	S36126	neural cell adhest
85	112.5	6.7	2029	1	TDFRLK	protein-tyrosine-p
86	112	6.6	946	1	A47299	for-related recept
87	112	6.6	976	2	T29583	hypothetical prote
88	112	6.6	1273	2	T42405	sax-3 protein - Ca
89	111	6.6	806	1	TVHUP3	fibroblast growth
90	111	6.6	6642	2	T29757	protein UNC-89 - C
91	110.5	6.5	349	2	A34815	carcinoembryonic a
92	110.5	6.5	518	2	JC4024	poliovirus recepto
93	110	6.5	459	2	S33766	platelet-derived g
94	110	6.5	917	2	I48950	telencephalin prec
95	110	6.5	1070	2	JC4593	protein-tyrosine k
96	110	6.5	1880	2	T18531	tracrin - medicina
97	110	6.5	2295	2	C68369	protein unc-52 (lm
98	109.5	6.5	338	2	JC1238	opioid-binding pro
99	109.5	6.5	345	2	JC1239	opioid-binding pro
100	109.5	6.5	526	2	S70587	butyrylcholin precu
101	109.5	6.5	1336	2	I60598	Fit-1 tyrosine kin
102	109	6.5	547	2	B45808	B-lymphocyte antig

103	109	6.5	646	2	I38049	cell surface glyco
104	108.5	6.4	345	2	S03199	oploid-binding pro
105	108.5	6.4	416	2	A54017	colon carcinoma-as
106	108.5	6.4	1328	2	T23007	hypothetical prote
107	108	6.4	526	2	A37821	butyrophilin - bov
108	107	6.3	773	1	QRRBG	secretory componen
109	106.5	6.3	354	1	S42938	proteoglycan link
110	106.5	6.3	1227	2	T23004	hypothetical prote
111	106.5	6.3	1232	2	T43027	neural cell adhesi
112	106	6.3	919	2	T32541	unc-5 protein - Ca
113	106	6.3	947	2	B44294	unc-5 protein, lon
114	106	6.3	1040	2	A57638	receptor tyrosine
115	106	6.3	1098	1	PFMGRB	platelet-derived g
116	106	6.3	1103	2	T22889	hypothetical prote
117	105.5	6.2	423	2	T29549	hypothetical prote
118	105.5	6.2	582	1	BNRT3S	myelin-associated
119	105.5	6.2	626	1	BNRT3	myelin-associated
120	105.5	6.2	662	2	C40862	heparin-binding gr
121	105.5	6.2	729	2	A56795	fibroblast growth
122	105.5	6.2	733	2	I49293	fibroblast growth
123	105.5	6.2	822	2	TVHFG	fibroblast growth
124	105.5	6.2	822	2	I49289	fibroblast growth
125	105.5	6.2	822	2	S29840	fibroblast growth
126	105.5	6.2	940	2	A40985	prolectin - fruit
127	104.5	6.2	268	2	T23555	hypothetical prote
128	104.5	6.2	392	2	B44194	poliovirus recepto
129	104.5	6.2	417	2	A44194	poliovirus recepto
130	104.5	6.2	1184	2	T09484	cartilage intermed
131	104.5	6.2	2222	2	TI3524	sdh protein - frul
132	104	6.2	299	1	AHRB	ig alpha chain C r
133	104	6.2	338	2	S09276	ig alpha chain C r
134	104	6.2	801	2	A48991	heparin-binding gr
135	104	6.2	801	2	I55363	fibroblast growth
136	104	6.2	828	2	I38912	receptor tyrosine
137	103.5	6.1	628	2	I38000	luteal blood gro
138	103.5	6.1	819	1	TVCFG	fibroblast growth
139	103.5	6.1	822	1	TVMSFG	fibroblast growth
140	103.5	6.1	824	2	S36439	fibroblast growth
141	103.5	6.1	832	2	JH0393	fibroblast growth
142	103.5	6.1	1356	2	TJ3402	protein-tyrosine k
143	103.5	6.1	1612	2	TJ0805	ducti protein - mo
144	103	6.1	811	2	A41054	fasciclin II, tran
145	103	6.1	873	2	B41054	fasciclin II p1-1
146	103	6.1	2783	2	T34416	hypothetical prote
147	102.5	6.1	318	2	F72171	K9R protein - vari
148	102.5	6.1	1176	2	JN0583	myosin-light-chain
149	102.5	6.1	1651	2	TI4160	transmembrane rece
150	102	6.0	637	2	B33785	myelin-associated
151	102	6.0	702	2	A36319	carcinoembryonic a
152	102	6.0	800	1	TVHUF	protein-tyrosine k
153	102	6.0	871	1	I48696	protein-tyrosine k
154	102	6.0	881	1	I48697	protein-tyrosine k
155	101.5	6.0	392	2	RMHUPD	poliovirus recepto
156	101.5	6.0	413	2	S65948	hemolin - cecropia
157	101.5	6.0	413	2	A37778	hemolin precursor
158	101.5	6.0	417	1	RMHUPA	poliovirus recepto
159	101.5	6.0	599	2	TI6774	hypothetical prote
160	101.5	6.0	898	2	A40114	fasciclin II precu
161	101.5	6.0	1260	1	S05479	neural cell adhesi
162	101	6.0	267	2	A38442	probable tumor sup
163	101	6.0	584	2	I50419	s-glycerin precuro
164	101	6.0	620	2	JH0593	Schwann cell myel
165	101	6.0	620	2	S38579	fibroblast growth
166	101	6.0	868	2	A46512	CD22 homolog/B lym
167	101	6.0	890	1	A53743	protein-tyrosine k
168	101	6.0	1742	2	S24600	prolectin - fruit
169	101	6.0	6831	2	A88852	protein unc-22 [lm
170	101	6.0	6839	2	S57242	twichin [leimlari
171	101	6.0	7160	2	T27935	hypothetical prote
172	100.5	6.0	355	1	LKCH	proteoglycan link
173	100.5	6.0	408	1	LKRT2	proteoglycan link
174	100.5	6.0	647	2	A35648	B-cell adhesion pr
175	100.5	6.0	700	1	HYHUMB	meprin A [EC 3.4.2
176	100.5	6.0	802	1	TVHUP4	fibroblast growth
177	100.5	6.0	847	2	JH0371	B-cell adhesion pr
178	100	5.9	354	1	LKRU	proteoglycan link
179	100	5.9	520	1	S44099	brain-derived neur
180	100	5.9	818	1	S44098	brain-derived neur
181	100	5.9	1021	2	I39207	leukocyte surface
182	99.5	5.9	459	2	A46254	CD4 precursor - ra
183	99.5	5.9	626	1	A61084	myelin-associated
184	99.5	5.9	790	2	A39627	protein-tyrosine k
185	99.5	5.9	1028	2	I58161	BiG-1 protein - ra
186	99.5	5.9	1379	2	UC4954	vascular endotheli
187	99.5	5.9	1666	2	A48594	skelamin - mouse
188	99	5.9	275	2	H35216	FP31 protein - fow
189	99	5.9	313	2	J01862	31R protein - vari
190	99	5.9	424	2	B35109	pregnancy-specific
191	99	5.9	458	1	RMHUT4	T-cell surface gly
192	99	5.9	773	2	T46283	hypothetical prote
193	99	5.9	812	1	A36477	fibroblast growth
194	99	5.9	818	2	UC4058	fibroblast growth
195	99	5.9	862	2	I49583	differentiation an
196	99	5.9	1375	2	TI3822	fraxzed gene prot
197	99	5.9	1526	2	TI3823	fraxzed gene prot
198	98.5	5.8	288	2	T24824	hypothetical prote
199	98.5	5.8	602	2	A45769	acetylcholine rece
200	98.5	5.8	1021	2	T42634	connectin/titin -
201	98.5	5.8	1330	2	S49010	embryonic receptor
202	98.5	5.8	1333	2	I78875	receptor tyrosine
203	98	5.8	880	1	UC4166	protein-tyrosine k
204	98	5.8	880	2	B53743	protein-tyrosine k
205	98	5.8	1499	2	I50212	protein-tyrosine-p
206	97.5	5.8	144	2	S36308	T-cell receptor de
207	97.5	5.8	354	1	S04243	proteoglycan link
208	97.5	5.8	476	1	A35104	brain-derived neur
209	97.5	5.8	588	2	I37202	B-CM protein - hu
210	97.5	5.8	729	2	A45120	fibroblast growth
211	97.5	5.8	764	2	A49448	irregular chiasm C
212	97.5	5.8	821	1	S06943	brain-derived neur
213	97.5	5.8	876	2	I49152	protein-tyrosine k
214	97.5	5.8	1348	2	AH1115	cell surface prote
215	97.5	5.8	1443	2	I50600	neogenin - chicken
216	97	5.7	116	2	D24891	T-cell receptor al
217	97	5.7	307	2	S55596	hypothetical prote
218	97	5.7	474	1	OMH18	alpha-1-B-glycopro
219	97	5.7	739	2	A41288	vascular cell adhe
220	97	5.7	751	2	T42597	DNA helicase/prima
221	97	5.7	824	2	S24108	protein-tyrosine k
222	97	5.7	1028	2	A53449	plasmacytoma-assoc
223	97	5.7	1147	2	A59307	myosin-light-chain
224	97	5.7	1274	2	S55050	cardiac myosin-bin
225	97	5.7	1367	2	A41228	protein-tyrosine k
226	97	5.7	1535	2	S46224	peroxidasin - frul
227	96.5	5.7	288	2	A31326	T-cell receptor de
228	96.5	5.7	313	2	T28598	hypothetical prote
229	96.5	5.7	772	2	T13078	KIAA0992 protein -
230	96.5	5.7	1200	2	TI7404	hyalin - sea urchi
231	96.5	5.7	2013	2	AD1129	probable peptidogl
232	96	5.7	243	2	S25755	Ig lambda chain -
233	96	5.7	407	2	C82428	glucose-1-phosphat
234	96	5.7	462	2	I38404	neu differentiatio
235	96	5.7	640	2	A43273	hearegulin precuro
236	96	5.7	739	2	JN0581	vascular cell adhe
237	96	5.7	1262	1	B48758	protein-tyrosine-p
238	96	5.7	1496	1	A48758	protein-tyrosine-p
239	96	5.7	1530	2	AH1396	peptidoglycan anch
240	96	5.7	6805	2	S20901	ctitin - rabblt (fr
241	95.5	5.7	243	2	A53244	leukocyte antigen
242	95.5	5.7	1132	2	A35089	myosin-binding pro
243	95	5.6	137	2	I46628	rearranged T-cell
244	95	5.6	814	1	A39752	fibroblast growth
245	95	5.6	994	2	I49276	c-ner tyrosine kin
246	95	5.6	1450	2	A44027	165k myofibrillar
247	95	5.6	1501	2	I58148	protein-tyrosine-p
248	95	5.6	1863	2	S46217	protein-tyrosine-p

249	95	5.6	1907	2	S50893	protein-tyrosine-p
250	95	5.6	1945	2	T13937	plexin A - fruit f
251	94.5	5.6	1335	2	S36314	T-cell receptor de
252	94.5	5.6	315	1	HNW24X	hemagglutinin prec
253	94.5	5.6	328	2	S30444	Sr2 protein - huma
254	94.5	5.6	477	1	I73631	brain-derived neur
255	94.5	5.6	588	2	JH0506	adhesion molecule
256	94.5	5.6	588	2	A45254	surface glycoprote
257	94.5	5.6	822	1	A56853	brain-derived neur
258	94.5	5.6	875	2	T33434	hypothetical prote
259	94.5	5.6	888	2	S23065	uto protein - mous
260	94.5	5.6	999	2	I38547	novel cellular pro
261	94.5	5.6	1256	2	T03096	CNO protein - rat
262	94	5.6	118	2	I71934	WIC class II T-A-a
263	94	5.6	268	2	A56446	Ig heavy chain V r
264	94	5.6	313	2	H36854	hemagglutinin - va
265	94	5.6	422	2	S32357	glial growth facto
266	94	5.6	583	2	G84829	probable PTR2 fami
267	94	5.6	887	2	AD2009	hypothetical prote
268	94	5.6	943	2	F69543	ATP-dependent RNA
269	94	5.6	1091	2	S01998	contactin precurs
270	94	5.6	1325	2	A64905	ylek protein - Esc
271	93.5	5.5	142	2	S36307	T-cell receptor de
272	93.5	5.5	259	2	JC7109	Sr2V protein - hum
273	93.5	5.5	329	1	A48754	B7-2 antigen - hum
274	93.5	5.5	587	2	JH0464	DN-GRASP precursor
275	93.5	5.5	799	2	S18209	fibroblast growth
276	93	5.5	432	1	RWC274	T-cell surface gly
277	93	5.5	435	2	D33258	pregnancy-specific
278	93	5.5	1018	2	JC4211	neural adhesion pr
279	93	5.5	1643	2	T14274	versican precursor
280	93	5.5	3381	2	T42389	versican precursor
281	92.5	5.5	144	2	S63322	T-cell receptor de
282	92.5	5.5	275	2	JC7604	CS86 spliced varia
283	92.5	5.5	424	2	A34595	pregnancy-specific
284	92.5	5.5	713	2	I50128	fibroblast growth
285	92.5	5.5	764	1	ORHUGS	secretory componen
286	92.5	5.5	1321	2	T00382	hypothetical prote
287	92	5.5	116	2	E24891	T-cell receptor al
288	92	5.5	132	2	A55410	Ig light chain V r
289	92	5.5	323	2	A48997	tumor surface anti
290	92	5.5	583	2	I39428	alcam - human
291	92	5.5	639	2	I61719	neu differentiation
292	92	5.5	829	2	JC4583	fibroblast growth
293	92	5.5	1005	2	T18537	Ig heavy chain - c
294	92	5.5	13055	2	T16580	hypothetical prote
295	91.5	5.4	240	2	JL0143	antigen BCM1 precu
296	91.5	5.4	330	2	A29915	teratocarcinoma gl
297	91.5	5.4	576	2	A32604	interleukin-1 rece
298	91.5	5.4	647	2	B41288	vascular cell adhe
299	91.5	5.4	1241	2	T37190	nephritin - human
300	91.5	5.4	2013	2	A11489	probable peptidogl
301	91	5.4	282	2	T17219	hypothetical prote
302	90.5	5.4	309	2	S15674	cell surface glyco
303	90.5	5.4	341	2	B95403	probable ABC trans
304	90.5	5.4	361	2	PN0020	fibroblast growth
305	90.5	5.4	474	1	C39667	brain-derived neur
306	90.5	5.4	476	1	B39667	brain-derived neur
307	90.5	5.4	487	2	S65133	butyrophilin - mou
308	90.5	5.4	631	1	A48346	cell fusion glycop
309	90.5	5.4	631	1	VGN2PD	cell fusion glycop
310	90.5	5.4	821	1	A39667	brain-derived neur
311	90.5	5.4	860	2	JC5702	EBB kinase activa
312	90.5	5.4	868	2	UC5701	EBB kinase activa
313	90	5.3	380	2	S12839	Ig heavy chain pre
314	90	5.3	526	2	T27581	hypothetical prote
315	90	5.3	789	2	T28714	hypothetical prote
316	90	5.3	821	1	TVHUY2	fibroblast growth
317	90	5.3	821	1	TVHUY2	contactin I precu
318	90	5.3	1018	2	A54744	contactin I precu
319	90	5.3	1240	2	T03097	CNO protein - huma
320	90	5.3	1343	2	B90893	hypothetical prote
321	90	5.3	1355	2	D85724	hypothetical prote
322					T87715	
322	89.5	5.3	142	2	S04664	T-cell receptor de
323	89.5	5.3	157	2	S04915	T-cell receptor de
324	89.5	5.3	243	2	A37982	calcium vector pro
325	89.5	5.3	275	2	A28928	pregnancy-specific
326	89.5	5.3	531	2	S20900	titin - mouse (fira
327	89.5	5.3	823	2	B35963	protein-tyrosine k
328	89.5	5.3	829	1	IJHICP	cadherin 3 precurs
329	89.5	5.3	1465	2	S43529	165K protein, skel
330	89.5	5.3	1483	2	C97012	probably celluloso
331	89	5.3	101	2	A29165	proteoglycan link
332	89	5.3	145	2	A29165	rearranged T-cell
333	89	5.3	279	2	S04693	T-cell receptor de
334	89	5.3	282	2	C28928	pregnancy-specific
335	89	5.3	413	1	IKC5A	colicin V secretio
336	89	5.3	523	2	I50478	neurotin - goldfis
337	89	5.3	682	2	A35969	heparin-binding gr
338	89	5.3	769	2	S16236	fibroblast growth
339	89	5.3	822	2	A45081	fibroblast growth
340	89	5.3	822	2	A41794	keratinocyte growt
341	89	5.3	1020	2	S05944	neutonal cell surf
342	88.5	5.2	524	2	S35341	ketin - fruit fly
343	88.5	5.2	3562	2	A47171	chondroitin sulfat
344	88	5.2	131	2	T20334	hypothetical prote
345	88	5.2	247	2	A55717	myelin/oligodendro
346	88	5.2	568	2	A45804	Ig mu chain C regi
347	88	5.2	850	2	JC5700	EBB kinase activa
348	88	5.2	1021	2	A57112	contactin precurs
349	88	5.2	1711	2	AB1183	peptidoglycan link
350	88	5.2	2051	2	T30938	receptor tyrosine
351	87.5	5.2	205	2	A48929	activated B-cell p
352	87.5	5.2	246	2	A47712	myelin/oligodendro
353	87.5	5.2	637	2	C43273	heregulin precurs
354	87.5	5.2	742	2	JS0326	alcohol dehydrogen
355	87.5	5.2	757	2	I45956	polymeric immunogl
356	87.5	5.2	1197	2	T30581	neural cell adhesi
357	87.5	5.2	1897	1	TDHUIK	leukocyte antigen-
358	87	5.2	139	2	S36302	T-cell receptor de
359	87	5.2	364	2	A30521	myeloid cell surfa
360	87	5.2	365	2	I72171	HLA-A*33.1, HLA-Aw
361	87	5.2	818	2	T19120	hypothetical prote
362	87	5.2	936	2	I40711	sapb protein - Cam
363	87	5.2	1451	2	S42167	190K protein - hum
364	86.5	5.1	115	2	C24891	T-cell receptor al
365	86.5	5.1	310	1	HNW2RA	hemagglutinin prec
366	86.5	5.1	353	2	JH0542	class I histocompa
367	86.5	5.1	465	2	A82211	MutT/nudix family
368	86.5	5.1	894	1	A41527	protein-tyrosine k
369	86.5	5.1	1348	2	S51656	vascular endotheli
370	86.5	5.1	1363	2	I58375	protein-tyrosine k
371	86.5	5.1	1637	2	T46438	hypothetical prote
372	86.5	5.1	1894	2	C54689	protein-tyrosine-p
373	86.5	5.1	2025	2	T21588	hypothetical prote
374	86.5	5.1	3157	2	B70969	probable PPE prote
375	86	5.1	116	2	B24891	T-cell receptor al
376	86	5.1	150	2	I46624	rearranged T-cell
377	86	5.1	270	2	A34636	Fe-gamma receptor
378	86	5.1	357	2	S09265	Ig alpha chain C r
379	86	5.1	357	2	S09265	Ig alpha chain C r
380	86	5.1	421	2	T46266	interleukin-1 rece
381	86	5.1	480	2	B56182	hypothetical prote
382	86	5.1	497	2	JC2456	pyruvate kinase (E
383	86	5.1	964	2	T15746	hypothetical prote
384	86	5.1	975	1	TVMSKT	hypothetical prote
385	86	5.1	1327	2	T09402	immunoglobulin-Ik
386	86	5.1	1345	2	H90975	hypothetical prote
387	86	5.1	1417	2	H90670	probable invasin f
388	86	5.1	1417	2	D85521	probable invasin e
389	86	5.1	2660	2	B85922	probable invasin Z
390	85.5	5.1	210	2	A56169	Ig kappa chain V r
391	85.5	5.1	216	2	JB0245	Ig lambda chain NI
392	85.5	5.1	218	2	S68241	Ig kappa chain V r
393	85.5	5.1	302	2	C36464	fibroblast growth
394	85.5	5.1	329	2	A44065	fibroblast growth

395	85.5	5.1	330	2	I46691	CD86 precursor - r
396	85.5	5.1	332	2	C83610	lactate-binding pr
397	85.5	5.1	388	2	B48899	beta-lactamase (EC
398	85.5	5.1	397	2	C43354	pregnancy-specific
399	85.5	5.1	419	2	TC4123	pregnancy-specific
400	85.5	5.1	677	2	SI4683	Ig mu chain precu
401	85.5	5.1	636	2	I61718	neu differentiatio
402	85.5	5.1	869	2	A86983	conserved hypoch
403	85.5	5.1	869	2	S72760	pspl protein - Myc
404	85.5	5.1	1094	2	S22573	DNA-directed DNA p
405	85.5	5.1	1518	2	S37328	probable purine nu
406	85.5	5.1	1691	1	D54689	protein-tyrosine-p
407	85.5	5.1	2541	2	T29340	hypothetical prote
408	85	5.0	104	2	S07705	T-cell receptor al
409	85	5.0	137	2	S36303	T-cell receptor de
410	85	5.0	166	2	A33402	pregnancy-specific
411	85	5.0	247	2	S58394	myelin/oligodendro
412	85	5.0	265	2	A55811	carcinoembryonic a
413	85	5.0	273	2	B28928	pregnancy-specific
414	85	5.0	428	2	I57486	pregnancy-specific
415	85	5.0	428	2	JS0032	pregnancy-specific
416	85	5.0	480	2	A56182	fibroblast growth
417	85	5.0	496	2	P00666	envelope protein -
418	85	5.0	769	1	QKRTGS	secretory componen
419	85	5.0	776	2	S41628	genome polypeptid
420	85	5.0	904	2	I38757	homolog of Drosoph
421	85	5.0	913	1	A47543	R-cadherin precurs
422	85	5.0	926	2	I38756	homolog of Drosoph
423	85	5.0	1005	2	A42265	alpha-mannosidase
424	85	5.0	2325	2	A61208	chondroitin sulfat
425	85	5.0	2409	1	A60979	glial growth factor
426	84.5	5.0	241	2	S32359	vertebral precursor
427	84.5	5.0	266	2	T29613	hypothetical prote
428	84.5	5.0	286	2	A28333	carcinoembryonic a
429	84.5	5.0	419	2	A33258	pregnancy-specific
430	84.5	5.0	419	2	A31135	pregnancy-specific
431	84.5	5.0	432	2	S30193	T-cell surface gly
432	84.5	5.0	436	2	B69371	bile acid-inducibl
433	84.5	5.0	457	2	A27449	T-cell surface gly
434	84.5	5.0	474	2	S15590	Ig heavy chain - h
435	84.5	5.0	568	2	I58106	gene DM-N9 protei
436	84.5	5.0	642	2	E72215	oligopeptide ABC t
437	84.5	5.0	795	2	T21487	hypothetical prote
438	84.5	5.0	821	1	TVMGBK	fibroblast growth
439	84.5	5.0	941	1	TVMTMD	protein-tyrosine k
440	84.5	5.0	980	1	TVCMTD	macrophage colony
441	84.5	5.0	1142	2	S36845	myosin-binding pro
442	84.5	5.0	1349	2	A11476	cell surface prote
443	84.5	5.0	1433	2	T30261	chitinase (EC 3.2.
444	84.5	5.0	2508	2	S61441	surface-associated
445	84	5.0	238	2	C90909	probable major tai
446	84	5.0	255	2	JC7593	SH2 domain-contai
447	84	5.0	315	1	HNWVVT	hemagglutinin prec
448	84	5.0	315	2	T37438	hemagglutinin - va
449	84	5.0	321	2	D39371	Ig V-region-like B
450	84	5.0	406	2	E43354	pregnancy-specific
451	84	5.0	452	1	MHHU	Ig mu chain C regi
452	84	5.0	453	2	S37768	Ig mu chain C regi
453	84	5.0	473	1	MHHUM	Ig mu chain C regi
454	84	5.0	621	2	B57431	myosin-binding C-P
455	84	5.0	781	2	S51592	Xyln precursor - R
456	84	5.0	939	2	AF2503	hypothetical prote
457	84	5.0	1065	2	H95321	NoIG efflux transp
458	84	5.0	1912	2	A56178	protein-tyrosine-p
459	84	5.0	2297	1	A55535	vertebral precursor
460	83.5	4.9	264	2	F27579	T-cell receptor
461	83.5	4.9	275	2	RWHUAC	T-cell receptor al
462	83.5	4.9	288	1	A45803	B-cell receptor
463	83.5	4.9	317	2	JI0118	Fc gamma (IgG) rec
464	83.5	4.9	329	2	AG0010	exported disulfate-b
465	83.5	4.9	339	2	S09264	Ig alpha chain C r
466	83.5	4.9	344	1	RWRTC2	T-cell surface gly
467	83.5	4.9	363	2	S07113	class I histocompa
468	83.5	4.9	372	2	C39371	Ig V-region-like B
469	83.5	4.9	496	2	S60685	envelope protein E
470	83.5	4.9	498	2	SI1246	LAG-3 protein prec
471	83.5	4.9	527	2	D75127	hypothetical prote
472	83.5	4.9	629	2	AE1525	probable peptidogl
473	83.5	4.9	705	2	S51635	fibroblast growth
474	83.5	4.9	707	2	A38429	keratinocyte growt
475	83.5	4.9	748	2	S41050	fibroblast growth
476	83.5	4.9	750	2	S41051	fibroblast growth
477	83.5	4.9	911	2	I56552	synapse-associated
478	83.5	4.9	987	2	A88746	protein C18P3.2 [l
479	83.5	4.9	1002	2	T19226	hypothetical prote
480	83.5	4.9	1028	2	C86364	protein C18B4.1 [l
481	83.5	4.9	1287	2	T30988	hypothetical prote
482	83.5	4.9	3698	1	GNMVHC	genome polypeptid
483	83	4.9	115	2	B32071	T-cell receptor de
484	83	4.9	233	2	S25747	Ig lambda chain -
485	83	4.9	422	2	B95001	conserved domain p
486	83	4.9	428	2	A27658	pregnancy-specific
487	83	4.9	445	2	A97873	conserved hypoch
488	83	4.9	977	2	S49004	tyrosine kinase Mp
489	83	4.9	1151	2	A45226	integrin alpha-1 c
490	83	4.9	3029	2	S76109	hypothetical prote
491	82.5	4.9	185	2	S37479	T-cell receptor al
492	82.5	4.9	218	2	JCS810	monoclonal antibod
493	82.5	4.9	218	2	B47712	myelin/oligodendro
494	82.5	4.9	229	2	A46527	B-cell-specific me
495	82.5	4.9	230	2	A56210	neu differentiatio
496	82.5	4.9	316	2	C37028	MHC class I histoc
497	82.5	4.9	353	2	S51242	heparin-binding f1
498	82.5	4.9	355	2	I80169	class I histocompa
499	82.5	4.9	356	1	S55437	translation releas
500	82.5	4.9	395	2	D43354	pregnancy-specific
501	82.5	4.9	417	2	A28277	pregnancy-specific
502	82.5	4.9	453	2	B83380	hypothetical prote
503	82.5	4.9	645	2	B43273	heretulin, splice
504	82.5	4.9	651	2	A96781	unknown protein p9
505	82.5	4.9	662	2	I61722	neu differentiatio
506	82.5	4.9	757	1	S48841	secretory componen
507	82.5	4.9	793	2	S59067	penton long fiber
508	82.5	4.9	822	2	S19947	fibroblast growth
509	82.5	4.9	822	2	B49151	fibroblast growth
510	82.5	4.9	942	2	S23251	protein-tyrosine k
511	82.5	4.9	975	2	T42576	probable envelope
512	82.5	4.9	1015	2	T32186	hypothetical prote
513	82.5	4.9	1648	2	S61654	probable membrane
514	82	4.9	147	2	I46625	rearranged T-cell
515	82	4.9	150	2	S36312	T-cell receptor de
516	82	4.9	242	2	S06942	hypothetical prote
517	82	4.9	250	2	H81854	probable zinc-bind
518	82	4.9	261	2	C85681	hypothetical prote
519	82	4.9	324	2	G43354	pregnancy-specific
520	82	4.9	326	2	F43354	pregnancy-specific
521	82	4.9	333	2	A43354	pregnancy-specific
522	82	4.9	335	2	A33514	pregnancy-specific
523	82	4.9	335	2	H43354	pregnancy-specific
524	82	4.9	340	2	T28137	Ig V-region-like B
525	82	4.9	352	2	S09266	Ig alpha chain C r
526	82	4.9	426	2	C55181	pregnancy-specific
527	82	4.9	426	2	S09016	pregnancy-specific
528	82	4.9	426	2	B35334	pregnancy-specific
529	82	4.9	436	2	B55181	pregnancy-specific
530	82	4.9	473	2	T35997	conserved hypoch
531	82	4.9	1086	2	AF1662	cellobiose-phospho
532	82	4.9	1160	2	F88369	protein unc-53 [lm
533	82	4.9	1185	2	D89824	hypothetical prote
534	82	4.9	1898	2	S46216	leukocyte antigen-
535	81.5	4.8	85	2	S08109	carcinoembryonic a
536	81.5	4.8	140	2	C24747	T-cell receptor (Ma
537	81.5	4.8	213	2	S68213	Ig heavy chain (Ma
538	81.5	4.8	235	2	I50610	T-cell surface gly
539	81.5	4.8	314	1	HNWVW	hemagglutinin prec
540	81.5	4.8	314	1	JQ1793	hemagglutinin prec

541	81.5	4.8	339	2	T28138	Ig V-region-like B	614	79.5	4.7	341	2	S16521	mitosis-specific c
542	81.5	4.8	426	2	A35954	pregnancy-specific	615	79.5	4.7	360	2	S09271	Ig alpha chain C r
543	81.5	4.8	630	1	UC1450	fibroblast growth	616	79.5	4.7	361	2	S68089	actin 2 - Arabidop
544	81.5	4.8	687	2	A49636	soluble vascular e	617	79.5	4.7	374	2	B82227	exodeoxyribonuclea
545	81.5	4.8	699	2	A12686	proteinaase II (imp	618	79.5	4.7	483	2	A97744	isocitrate dehydro
546	81.5	4.8	699	2	E97468	dipeptidyl aminope	619	79.5	4.7	493	2	A55181	pregnancy-specific
547	81.5	4.8	707	2	A54846	fibroblast growth	620	79.5	4.7	610	2	A55939	dihydroliposamide S
548	81.5	4.8	822	2	B54846	fibroblast growth	621	79.5	4.7	637	2	T49099	dihydroliposamide S
549	81.5	4.8	1015	2	T32984	hypothetical prote	622	79.5	4.7	701	2	T17243	hypothetical prote
550	81.5	4.8	1462	1	A69809	probable multifunc	623	79.5	4.7	878	2	A83748	endo-beta-N-acetyl
551	81.5	4.8	3507	2	T34513	hypothetical prote	624	79.5	4.7	974	2	S34189	starch phosphoryla
552	81	4.8	117	2	S49983	recll receptor alp	625	79.5	4.7	1209	2	T14357	neural cell adhesi
553	81	4.8	139	2	T46630	rearranged T-cell	626	79.5	4.7	1265	1	A37967	complement C3 prec
554	81	4.8	145	2	T46631	rearranged T-cell	627	79.5	4.7	1663	1	C3R	Ig lambda chain pr
555	81	4.8	206	2	A40305	hemagglutinin prec	628	79	4.7	118	2	S04519	T-cell receptor be
556	81	4.8	315	1	HNZVZV	Ig heavy chain - R	629	79	4.7	132	2	PQ0060	pregnancy-specific
557	81	4.8	381	2	I51174	probable advanced	630	79	4.7	210	2	UC4122	herregulin precurs
558	81	4.8	402	2	T09062	T-cell surface gly	631	79	4.7	241	2	D43273	vascular cell adhe
559	81	4.8	432	1	RWMT4	hypothetical prote	632	79	4.7	345	2	A46052	aggrecan - pig (fr
560	81	4.8	438	2	E96545	matrix, capaid, nu	633	79	4.7	370	2	S29139	Oxfl protein - chl
561	81	4.8	449	2	A45357	98g protein - cell	634	79	4.7	374	2	A46132	hypothetical prote
562	81	4.8	450	2	S25162	S88 binding protei	635	79	4.7	407	2	T08732	cellular hepatitis
563	81	4.8	509	2	JC6203	hypothetical prote	636	79	4.7	451	2	S71754	cyclin A-like prot
564	81	4.8	767	2	F86383	zC21.2 protein - C	637	79	4.7	502	2	T02746	lymphocyte antigen
565	81	4.8	823	2	S44873	bacillopeptidase F	638	79	4.7	567	2	S29498	77.8k DNA helicase
566	81	4.8	1433	1	A36724	protein U - Yersin	639	79	4.7	716	1	WZBBE6	probable two-compo
567	81	4.8	1492	2	T14652	phase lambda-d-relat	640	79	4.7	741	2	B83265	hypothetical prote
568	81	4.8	1545	2	T14966	dominant autoantig	641	79	4.7	742	2	F84643	nematodes resistan
569	81	4.8	1650	2	S53457	T cell receptor Ck	642	79	4.7	1255	2	T06267	protein-tyrosine k
570	80.5	4.8	133	2	S57870	Vvreb protein prec	643	79	4.7	1315	2	T28679	chromodomain bindi
571	80.5	4.8	142	2	B28344	MHC class I histoc	644	79	4.7	1388	2	T38720	genome polypeptide
572	80.5	4.8	366	2	I37523	pregnancy-specific	645	79	4.7	3414	1	GNWVNE	T-cell receptor be
573	80.5	4.8	426	2	B33258	pregnancy-specific	646	79	4.7	136	2	UC0473	sodium channel bet
574	80.5	4.8	426	2	A35341	hypothetical prote	647	79	4.7	136	2	S36320	Ig kappa chain - s
575	80.5	4.8	441	2	T31482	interleukin-2 rece	648	78.5	4.7	215	2	A57843	T-cell receptor al
576	80.5	4.8	551	2	A30342	fibroblast growth	649	78.5	4.7	230	2	S33161	basigin precursor
577	80.5	4.8	820	2	S17295	hypothetical prote	650	78.5	4.7	259	2	S57494	mucin 5Ac (clone J
578	80.5	4.8	874	2	T29548	MAP kinase kinase	651	78.5	4.7	270	2	S65739	integrin-associat
579	80.5	4.8	1216	2	S60613	conserved hypochet	652	78.5	4.7	279	2	S53363	inositol monophosp
580	80.5	4.8	1493	2	T10757	insulin-like growt	653	78.5	4.7	335	2	A75363	class I histocompa
581	80.5	4.8	1641	2	D82704	rearranged T-cell	654	78.5	4.7	335	2	S36646	MHC class I histoc
582	80.5	4.8	2482	2	I48922	hypothetical prote	655	78.5	4.7	335	2	A75363	MHC class I histoc
583	80.5	4.8	2483	1	A49617	cell surface glyco	656	78.5	4.7	335	2	I80171	conserved hypochet
584	80	4.7	124	2	F03560	probable type II s	657	78.5	4.7	355	2	S03537	pregnancy-specific
585	80	4.7	133	2	I46632	rearranged T-cell	658	78.5	4.7	366	2	I37544	Ig heavy chain pre
586	80	4.7	147	2	S25499	T-cell receptor al	659	78.5	4.7	366	2	S42823	E-selectin precurs
587	80	4.7	194	2	T29925	hypothetical prote	660	78.5	4.7	366	2	B37028	DNA ligase (ATP) (
588	80	4.7	218	2	A36040	Ig heavy chain V-I	661	78.5	4.7	407	2	C83589	probable lipoprote
589	80	4.7	287	2	S71192	mitosis-specific c	662	78.5	4.7	419	2	B54312	cadherin 4 precurs
590	80	4.7	304	1	RKCH7	cell surface glyco	663	78.5	4.7	568	2	A34891	hypothetical prote
591	80	4.7	365	2	A45847	MHC class I histoc	664	78.5	4.7	612	2	B42755	protein-tyrosine-p
592	80	4.7	549	2	S04845	Ig heavy chain pre	665	78.5	4.7	787	2	A29066	sex factor aggrega
593	80	4.7	684	2	F97148	aldenhyde:ferredoxi	666	78.5	4.7	916	2	S73873	probable membrane
594	80	4.7	707	2	JC7763	neural leucine-r	667	78.5	4.7	916	2	C38992	hyperplastic discs
595	80	4.7	748	2	T37097	probable secreted	668	78.5	4.7	1059	2	T25245	hypothetical prote
596	80	4.7	893	2	A37284	surface-arry prote	669	78.5	4.7	1188	1	A57064	hypothetical prote
597	80	4.7	939	2	A82275	hypothetical prote	670	78.5	4.7	1243	1	S60138	endo-beta-N-acetyl
598	80	4.7	999	2	S72267	Ca2+-transporting	671	78.5	4.7	1609	2	S25345	starch phosphoryla
599	80	4.7	1123	2	S36846	myosin-binding pro	672	78.5	4.7	2895	2	T08437	neural cell adhesi
600	80	4.7	1582	2	T15308	hypothetical prote	673	78.5	4.7	4006	2	T09070	complement C3 prec
601	80	4.7	2481	2	A43908	fibronectin - Afri	674	78	4.6	95	2	B98068	Ig lambda chain pr
602	80	4.7	3488	2	T34418	hypothetical prote	675	78	4.6	121	2	A29080	T-cell receptor al
603	79.5	4.7	104	2	S36305	T-cell receptor de	676	78	4.6	309	2	I49503	B-lymphocyte activ
604	79.5	4.7	114	2	JH0341	T-cell receptor al	677	78	4.6	335	2	C54312	pregnancy-specific
605	79.5	4.7	135	2	S36298	T-cell receptor de	678	78	4.6	336	2	S42632	Fit-1S protein pre
606	79.5	4.7	137	2	C45893	T-cell receptor al	679	78	4.6	342	2	E71101	probable geranylge
607	79.5	4.7	140	2	I46638	rearranged T-cell	680	78	4.6	367	2	AE3303	putrescine-binding
608	79.5	4.7	147	2	T46623	rearranged T-cell	681	78	4.6	508	2	A33378	fasciclin III prec
609	79.5	4.7	232	2	S25756	Ig lambda chain -	682	78	4.6	592	2	S25705	Ig mu chain - shee
610	79.5	4.7	254	2	C42691	fibroblast growth	683	78	4.6	617	2	B64734	yach protein - Eec
611	79.5	4.7	289	2	G00031	MHC class I histoc	684	78	4.6	684	2	S60266	novel antigen rece
612	79.5	4.7	313	2	I36958	Ig alpha chain C r	685	78	4.6	841	2	JC5894	killer cell inhibi
613	79.5	4.7	335	2	S09275	Ig alpha chain C r	686	78	4.6	886	2	S29605	glycoprotein 350/2

687	78	4.6	1185	2	A42404	collagen adhesin -
688	78	4.6	1203	2	T04294	hypothetical prote
689	78	4.6	1273	1	T08RT1	leukocyte common a
690	78	4.6	3848	2	T17414	tipc protein - sll
691	78	4.6	4116	2	T13719	calo protein - fru
692	77.5	4.6	103	2	S36067	Ig lambda chain -
693	77.5	4.6	104	2	G24402	T-cell receptor al
694	77.5	4.6	122	2	S16439	Ig lambda chain -
695	77.5	4.6	134	2	A45893	T-cell receptor al
696	77.5	4.6	182	2	T83053	pregnancy-specific
697	77.5	4.6	226	2	S25745	Ig lambda chain -
698	77.5	4.6	227	2	A33937	Ig light chain (13
699	77.5	4.6	235	2	S25758	Ig lambda chain -
700	77.5	4.6	240	2	JC4121	pregnancy-specific
701	77.5	4.6	288	2	S26690	Ig heavy chain VDJ
702	77.5	4.6	295	2	A37412	T-cell receptor de
703	77.5	4.6	332	2	JN0067	pregnancy-specific
704	77.5	4.6	363	1	S42102	MHC class I histoc
705	77.5	4.6	364	2	S59931	glycerophosphodies
706	77.5	4.6	364	2	S59932	glycerophosphodies
707	77.5	4.6	364	2	S59933	glycerophosphodies
708	77.5	4.6	364	2	A43576	glycerophosphodies
709	77.5	4.6	364	2	S59934	glycerophosphodies
710	77.5	4.6	420	2	H84182	hypothetical prote
711	77.5	4.6	436	2	S60686	envelope protein E
712	77.5	4.6	509	2	S17597	Ig delta chain (W1
713	77.5	4.6	537	2	A46611	myosin-binding pro
714	77.5	4.6	542	2	S49219	fiber protein - ca
715	77.5	4.6	662	2	T16525	hypothetical prote
716	77.5	4.6	704	2	A48040	mepirin A (BC 3.4.2
717	77.5	4.6	1009	2	T18533	CryIac toxin-bindi
718	77.5	4.6	1036	2	B69368	hypothetical prote
719	77.5	4.6	1047	2	T41343	probable translati
720	77.5	4.6	1141	2	B89824	hypothetical prote
721	77.5	4.6	1987	1	S12050	protein-tyrosine-p
722	77	4.6	95	2	D95201	hypothetical prote
723	77	4.6	113	2	JH0340	T-cell receptor al
724	77	4.6	135	2	S26512	T-cell receptor al
725	77	4.6	146	2	S36323	T-cell receptor de
726	77	4.6	309	2	T15747	hypothetical prote
727	77	4.6	311	2	T31517	hypothetical prote
728	77	4.6	356	2	F71624	rifin PFB0060w - m
729	77	4.6	396	2	T45033	hypothetical prote
730	77	4.6	400	1	A39822	leukostialin precu
731	77	4.6	403	2	I52590	m33-B isoform - mo
732	77	4.6	430	2	T28143	tapasin 1 homolog,
733	77	4.6	433	2	T17289	hypothetical prote
734	77	4.6	462	2	A41158	dipeptidyl-peptida
735	77	4.6	496	2	A43383	envelope glycoprot
736	77	4.6	590	2	I56526	interleukin 1 rece
737	77	4.6	630	2	T51281	beta-D-glucan exoh
738	77	4.6	639	2	T20772	hypothetical prote
739	77	4.6	661	2	B54078	methyl-accepting c
740	77	4.6	680	2	JC5895	Killer cell inhibi
741	77	4.6	690	2	G84638	hypothetical prote
742	77	4.6	800	2	AB1129	internatin A [impo
743	77	4.6	846	2	T19179	hypothetical prote
744	77	4.6	1666	2	T38393	clathrin heavy cha
745	77	4.6	2491	1	A28372	insulin-like growt
746	76.5	4.5	114	2	I38316	T-cell receptor de
747	76.5	4.5	115	2	S03513	T-cell receptor de
748	76.5	4.5	120	2	S36306	T-cell receptor de
749	76.5	4.5	151	2	I46626	rearranged T-cell
750	76.5	4.5	239	2	G97165	flagellar hook ass
751	76.5	4.5	240	2	S01299	OX-45 membrane gly
752	76.5	4.5	240	2	A39016	T-cell surface gly
753	76.5	4.5	255	2	JQ1240	hypothetical 29.3k
754	76.5	4.5	266	2	B39581	GRSAG protein 9u
755	76.5	4.5	318	2	H75157	daunorubicin resis
756	76.5	4.5	336	2	I48471	Pc gamma (Igg) rec
757	76.5	4.5	477	2	H75026	oligopeptide abc c
758	76.5	4.5	530	2	T18596	hypothetical prote
759	76.5	4.5	742	2	S38093	probable purine nu

760	76.5	4.5	771	2	A83348	probable aldehyde
761	76.5	4.5	874	2	C84513	Mutator-like trans
762	76.5	4.5	1110	2	T19673	hypothetical prote
763	76.5	4.5	1138	2	S24614	myosin-binding pro
764	76.5	4.5	1350	2	AF2005	RNA polymerase bet
765	76.5	4.5	1365	2	T30198	alkaline phosphata
766	76.5	4.5	1832	2	T31113	mucin-like glycopr
767	76	4.5	120	2	C26945	T-cell receptor de
768	76	4.5	133	2	P24402	T-cell receptor al
769	76	4.5	141	2	S36318	T-cell receptor de
770	76	4.5	145	2	S25743	Ig lambda chain -
771	76	4.5	149	2	S36317	T-cell receptor de
772	76	4.5	323	2	S06946	Fc gamma (Igg) rec
773	76	4.5	341	2	S26686	CAMP response elem
774	76	4.5	360	2	A27638	MHC class I histoc
775	76	4.5	362	2	I72755	HLA-B*5602 - human
776	76	4.5	362	2	I72754	HLA-B*5601 - human
777	76	4.5	365	2	I38439	MHC class I histoc
778	76	4.5	366	2	I81231	lymphocyte antigen
779	76	4.5	400	2	AD3364	probable acyl-CoA
780	76	4.5	401	2	AG3552	branched-chain am
781	76	4.5	415	2	AB3637	alpha-methylacyl-C
782	76	4.5	441	2	H96817	hypothetical prote
783	76	4.5	443	2	A96818	hypothetical prote
784	76	4.5	446	2	F84451	probable uridylyl
785	76	4.5	457	1	RMNST4	T-cell surface gly
786	76	4.5	478	2	AP1758	chitinase and chit
787	76	4.5	496	2	PC4408	protein B - Tick-b
788	76	4.5	562	2	A65166	hypothetical 63.2k
789	76	4.5	562	2	B91194	probable enzyme [1
790	76	4.5	562	2	C86041	probable enzyme y1
791	76	4.5	609	2	T16135	hypothetical prote
792	76	4.5	649	2	T32755	hypothetical prote
793	76	4.5	800	2	S37387	internatin A precu
794	76	4.5	959	1	P2XR13	outer capsid prote
795	76	4.5	1032	2	T34433	hypothetical prote
796	76	4.5	1497	2	I49607	procollagen type V
797	76	4.5	2232	2	T34434	hypothetical prote
798	76	4.5	3716	2	E70969	probable PPG prote
799	76	4.5	4660	2	T43737	gp330 protein prec
800	75.5	4.5	116	2	S22558	Ig heavy chain V r
801	75.5	4.5	146	2	H32536	T-cell receptor al
802	75.5	4.5	275	2	PS0402	basigin type III -
803	75.5	4.5	283	2	F87183	probable ecto
804	75.5	4.5	297	2	AG2955	hypothetical prote
805	75.5	4.5	297	2	F98327	hypothetical prote
806	75.5	4.5	312	2	H64560	probable tetraacyl
807	75.5	4.5	342	2	A45966	Ig alpha chain C r
808	75.5	4.5	366	2	I37527	MHC class I histoc
809	75.5	4.5	371	2	A53908	brevican precursor
810	75.5	4.5	398	2	A39371	Ig V-region-like B
811	75.5	4.5	484	2	B64481	hypothetical prote
812	75.5	4.5	549	2	G68618	dipeptide ABC tran
813	75.5	4.5	607	2	A95122	Ths522, relaxase [
814	75.5	4.5	705	1	CIHRUB	complement subcomp
815	75.5	4.5	742	2	A49340	alcohol dehydrogen
816	75.5	4.5	769	2	E90158	AAA family Arpase
817	75.5	4.5	796	2	T20393	hypothetical prote
818	75.5	4.5	937	2	A45082	neurotrophic recep
819	75.5	4.5	1042	2	AF0739	exodeoxyribonuclea
820	75.5	4.5	1294	2	T04278	hypothetical prote
821	75.5	4.5	1662	2	T01893	hypothetical prote
822	75.5	4.5	1902	2	C97702	cell surface antig
823	75	4.4	132	1	RMMSAV	T-cell receptor al
824	75	4.4	141	2	S38389	T-cell receptor be
825	75	4.4	233	2	S25744	Ig lambda chain -
826	75	4.4	234	2	S01320	Ig kappa chain pre
827	75	4.4	238	2	D90876	major tail protein
828	75	4.4	252	2	H72554	probable Rieseke pr
829	75	4.4	262	2	C85692	probable tail comp
830	75	4.4	301	2	AC3476	probable proteinas
831	75	4.4	335	2	B33251	nonpeptide cross-
832	75	4.4	346	2	C81088	alcohol dehydrogen

Probable aldehyde
 Mutator-like trans
 hypothetical prote
 myosin-binding pro
 RNA polymerase bet
 alkaline phosphata
 mucin-like glycopr
 T-cell receptor de
 T-cell receptor al
 T-cell receptor de
 Ig lambda chain -
 T-cell receptor de
 Fc gamma (Igg) rec
 CAMP response elem
 MHC class I histoc
 HLA-B*5602 - human
 HLA-B*5601 - human
 MHC class I histoc
 lymphocyte antigen
 probable acyl-CoA
 branched-chain am
 alpha-methylacyl-C
 hypothetical prote
 hypothetical prote
 probable uridylyl
 T-cell surface gly
 chitinase and chit
 protein B - Tick-b
 hypothetical 63.2k
 probable enzyme [1
 probable enzyme y1
 hypothetical prote
 hypothetical prote
 internatin A precu
 outer capsid prote
 hypothetical prote
 procollagen type V
 hypothetical prote
 probable PPG prote
 gp330 protein prec
 Ig heavy chain V r
 T-cell receptor al
 basigin type III -
 probable ecto
 hypothetical prote
 hypothetical prote
 probable tetraacyl
 Ig alpha chain C r
 MHC class I histoc
 brevicin precursor
 Ig V-region-like B
 hypothetical prote
 dipeptide ABC tran
 Ths522, relaxase [
 complement subcomp
 alcohol dehydrogen
 AAA family Arpase
 hypothetical prote
 neurotrophic recep
 exodeoxyribonuclea
 hypothetical prote
 hypothetical prote
 cell surface antig
 T-cell receptor al
 T-cell receptor be
 Ig lambda chain -
 Ig kappa chain pre
 major tail protein
 probable Rieseke pr
 probable tail comp
 probable proteinas
 nonpeptide cross-
 alcohol dehydrogen

833	75	4.4	360	2	AE1931	hypothetical prote
834	75	4.4	362	2	I37120	MHC class I histoc
835	75	4.4	362	2	B30345	MHC class I histoc
836	75	4.4	362	2	I37522	MHC class I histoc
837	75	4.4	362	2	I61904	MHC class I histoc
838	75	4.4	362	2	I54457	MHC class I lympho
839	75	4.4	362	2	A30345	MHC class I histoc
840	75	4.4	367	2	H65132	hypothetical 44.3
841	75	4.4	391	1	MHUBT	Ig mu heavy chain
842	75	4.4	396	2	C95088	S-adenosylmethioni
843	75	4.4	396	2	G97955	methionine adenosy
844	75	4.4	450	1	FOLJPP	gag polyprotein -
845	75	4.4	450	1	S23819	gag protein - feli
846	75	4.4	471	2	B38637	Ras inhibitor (clo
847	75	4.4	483	2	A69745	hypothetical prote
848	75	4.4	496	2	PQ0508	envelope glycoprot
849	75	4.4	496	2	E90181	hypothetical prote
850	75	4.4	507	2	AE0473	colicin (partial)
851	75	4.4	555	2	T01142	hypothetical prote
852	75	4.4	563	2	A70038	L-lactate permease
853	75	4.4	589	2	A34341	poly(3)-hydroxybuty
854	75	4.4	600	2	A82043	inner membrane cop
855	75	4.4	630	2	F85074	hypothetical prote
856	75	4.4	632	2	S73431	MG288 homolog D09
857	75	4.4	673	2	S46520	luciferin-binding
858	75	4.4	686	2	JC7569	Delta-4 protein -
859	75	4.4	808	2	T23129	hypothetical prote
860	75	4.4	997	2	A40812	Ca2+-transporting
861	75	4.4	999	2	A34307	Ca2+-transporting
862	75	4.4	1042	2	B40812	endo-1,4-beta-xyla
863	75	4.4	1234	2	S72640	genome, polyprotein
864	75	4.4	1241	2	S26373	synaptic scafoldi
865	75	4.4	1277	2	T14152	probable cell surf
866	75	4.4	1622	2	AE1717	probable peptidogl
867	75	4.4	2109	1	I50421	aggreccan precursor
868	75	4.4	2134	2	A28452	aggreccan precursor
869	75	4.4	2132	1	A55182	aggreccan precursor
870	75	4.4	2145	1	A39086	aggreccan precursor
871	75	4.4	3216	2	C90538	hypothetical prote
872	75	4.4	3263	2	B82410	large repetitive p
873	75	4.4	3624	2	AD0835	T-cell receptor al
874	75	4.4	115	2	A24891	T-cell receptor be
875	74.5	4.4	131	2	PQ0059	T-cell receptor al
876	74.5	4.4	133	2	S57885	T-cell receptor al
877	74.5	4.4	135	1	RMHUV	YbDQ protein - Bsc
878	74.5	4.4	142	1	E64794	hypothetical prote
879	74.5	4.4	142	2	P90709	hypothetical prote
880	74.5	4.4	142	2	B85560	hypothetical prote
881	74.5	4.4	208	2	B49444	Ig lambda chain (N
882	74.5	4.4	212	2	C33258	pregnancy-specific
883	74.5	4.4	235	2	AD1735	hypothetical prote
884	74.5	4.4	235	2	T05381	probable heme expo
885	74.5	4.4	345	2	C72760	MHC class I histoc
886	74.5	4.4	361	2	I50107	hypothetical prote
887	74.5	4.4	361	2	B90461	MHC class I histoc
888	74.5	4.4	366	1	HLHMW3	MHC class I histoc
889	74.5	4.4	377	2	A49885	surface antigen -
890	74.5	4.4	445	2	S43492	exodeoxyribonuclea
891	74.5	4.4	476	2	A10189	hypothetical prote
892	74.5	4.4	503	2	AB1933	hypothetical prote
893	74.5	4.4	625	2	T16777	DNA-directed RNA p
894	74.5	4.4	652	2	G96560	hypothetical prote
895	74.5	4.4	717	2	B32858	interleukin-4 rece
896	74.5	4.4	732	2	A43315	neurotrophic recep
897	74.5	4.4	810	1	A33380	Tomb-dependent rec
898	74.5	4.4	943	2	B45082	mitotic control pr
899	74.5	4.4	946	2	B87316	calbiothiole-phospho
900	74.5	4.4	1000	2	JB0110	probable membrane
901	74.5	4.4	1086	2	AH1290	hypothetical prote
902	74.5	4.4	1302	2	AC2574	hypothetical prote
903	74.5	4.4	1333	2	S63403	hypothetical prote
904	74.5	4.4	1356	2	T16718	hypothetical prote
905	74.5	4.4	1356	2	T16718	hypothetical prote
906	74.5	4.4	1446	2	T13018	hypothetical prote
907	74.5	4.4	1615	2	C75551	glutamate synthase
908	74.5	4.4	2143	2	G96595	hypothetical prote
909	74.5	4.4	3890	2	C89921	hypothetical prote
910	74.5	4.4	4436	2	B71086	hypothetical prote
911	74	4.4	115	2	A30583	T-cell receptor de
912	74	4.4	130	2	S08079	Ig kappa chain pre
913	74	4.4	143	2	S36321	T-cell receptor de
914	74	4.4	145	2	S36299	T-cell receptor de
915	74	4.4	217	2	UE0246	Ig lambda chain NI
916	74	4.4	264	2	T26976	hypothetical prote
917	74	4.4	270	1	S77085	molybdate-binding
918	74	4.4	318	2	C71197	probable ATP-bind
919	74	4.4	327	2	P87544	UDP-glucose 4-epim
920	74	4.4	330	2	AE3119	ABC transporter, s
921	74	4.4	341	2	S20827	CAMP response elem
922	74	4.4	351	2	S78042	Ig mu chain C regi
923	74	4.4	353	2	C86932	conserved hypochet
924	74	4.4	354	2	S24436	class I histocompa
925	74	4.4	362	2	I56130	HLA-B*5401 - human
926	74	4.4	362	2	I59633	MHC HLA-B transmem
927	74	4.4	362	2	I72753	HLA-B*3502 - human
928	74	4.4	362	2	S24434	class I histocompa
929	74	4.4	362	2	I72752	HLA-B*5501 - human
930	74	4.4	362	2	I56133	MHC class I protei
931	74	4.4	365	2	B95260	recf protein (limp
932	74	4.4	365	2	B98125	recombination prot
933	74	4.4	387	2	B98168	periplasmic-iron-b
934	74	4.4	425	2	E71982	isocitrate dehydro
935	74	4.4	430	2	S50981	probable membrane
936	74	4.4	487	2	AD3643	adhesion aid-I (lm
937	74	4.4	509	2	JC5288	SHP substrate-1 pr
938	74	4.4	513	2	JC5289	SHP substrate-1 pr
939	74	4.4	517	2	B87644	4-comarate-CoA li
940	74	4.4	555	2	T47573	hypothetical prote
941	74	4.4	570	2	A90644	peptide transport-
942	74	4.4	617	2	A90644	probable membrane
943	74	4.4	617	2	A85495	probable membrane
944	74	4.4	626	2	I38618	zinc finger protei
945	74	4.4	628	2	T51283	glucan 1,3-beta-gl
946	74	4.4	635	2	JC5896	killer cell inhibi
947	74	4.4	640	2	B84478	probable replicati
948	74	4.4	642	2	S58154	hypothetical prote
949	74	4.4	666	2	H89581	protein dim-1 (limp
950	74	4.4	708	2	T19474	hypothetical prote
951	74	4.4	899	2	AG0859	outer membrane ush
952	74	4.4	1020	2	A46405	C protein alpha an
953	74	4.4	1144	2	D97227	pyruvate carboxyla
954	74	4.4	1251	2	T21389	hypothetical prote
955	74	4.4	1452	1	S17670	protein-tyrosine-p
956	74	4.4	1537	2	JC4172	DNA (cytosine-5-)-
957	74	4.4	1763	2	T17465	riifamycin polyketi
958	74	4.4	3412	1	GNWV7B	genome polyprotein
959	74	4.4	106	2	PL0267	Ig kappa chain V r
960	73.5	4.4	108	1	KVRH85	Ig kappa chain V r
961	73.5	4.4	111	1	L6HUST	Ig lambda chain V r
962	73.5	4.4	111	2	JH0339	T-cell receptor al
963	73.5	4.4	229	2	A20969	Ig kappa chain pre
964	73.5	4.4	245	2	T18609	hypothetical prote
965	73.5	4.4	246	2	S38950	Ig gamma chain - m
966	73.5	4.4	253	2	T15475	hypothetical prote
967	73.5	4.4	257	2	PS0401	basigin type II -
968	73.5	4.4	271	2	S43512	GP42/Baafign prote
969	73.5	4.4	273	2	UX0107	basigin precursor
970	73.5	4.4	283	1	PCMSG1	Fc gamma (1g) rec
971	73.5	4.4	291	2	T30488	hypothetical prote
972	73.5	4.4	304	2	B88746	protein C18F3.3 (l
973	73.5	4.4	310	2	JL0119	Fc gamma (1g) rec
974	73.5	4.4	316	2	H71231	molybdopterin bios
975	73.5	4.4	325	2	I54449	MHC class I HLA-Cx
976	73.5	4.4	330	2	A40071	Fc gamma (1g) rec
977	73.5	4.4	330	2	I49660	Fc-gamma-1/gamma-2
978	73.5	4.4	339	2	JC7509	glycoprotein VI-1

979	73.5	4.4	348	2	S09273	Ig alpha chain C r	1052	73	4.3	362	2	I84490	lymphocyte antigen
980	73.5	4.4	351	2	B34595	pregnanone-specific	1053	73	4.3	362	2	A45880	MHC class I histoc
981	73.5	4.4	351	2	A97064	D-mannanase hydrol	1054	73	4.3	362	2	I54442	MHC class I histoc
982	73.5	4.4	357	2	D82337	UDP-N-acetylenolip	1055	73	4.3	365	2	I37482	MHC class I histoc
983	73.5	4.4	352	2	S68090	actin 8 - Arabidop	1056	73	4.3	378	2	S41870	surface antigen -
984	73.5	4.4	366	2	I68712	MHC class I histoc	1057	73	4.3	426	2	C72166	A22R protein - var
985	73.5	4.4	366	2	F72062	hypothetical prote	1058	73	4.3	489	2	T09151	glutathione-dioluf
986	73.5	4.4	366	2	A86561	CT449 hypothetical	1059	73	4.3	499	2	E86782	D-alanine activat
987	73.5	4.4	400	2	T34363	hypothetical prote	1060	73	4.3	507	2	A46661	cystathionine beta
988	73.5	4.4	404	2	A46480	Fe gamma (196) rec	1061	73	4.3	508	2	B91250	hypothetical prote
989	73.5	4.4	408	2	F81252	NADH2 dehydrogenas	1062	73	4.3	521	2	B84746	hypothetical prote
990	73.5	4.4	427	2	F64064	colB protein - Hae	1063	73	4.3	580	2	AE1088	ABC transporter, A
991	73.5	4.4	446	2	S40295	Ig gamma-2a chain	1064	73	4.3	615	2	T20839	hypothetical prote
992	73.5	4.4	451	2	T30603	perlecan homolog 2	1065	73	4.3	681	2	A45055	glutamine-fructose
993	73.5	4.4	482	2	T22754	hypothetical prote	1066	73	4.3	694	2	F97279	Delta-4 protein -
994	73.5	4.4	551	2	G84301	hypothetical prote	1067	73	4.3	694	2	F97279	TPR-repeat-contain
995	73.5	4.4	554	2	C70512	hypothetical prote	1068	73	4.3	865	2	B85075	probable achilla tr
996	73.5	4.4	555	2	D71444	probable thioester	1069	73	4.3	886	2	S42841	T16612.1 protein -
997	73.5	4.4	568	2	A89958	acetyl-CoA synthet	1070	73	4.3	913	2	IJCCHR	R-cadherin precurs
998	73.5	4.4	650	2	S22835	alpha-agglutinin -	1071	73	4.3	954	2	AI0438	probable exported
999	73.5	4.4	659	2	G91009	hypothetical prote	1072	73	4.3	974	1	URHDP	peptidylglycine mo
1000	73.5	4.4	659	2	G91009	colicin I receptor	1073	73	4.3	977	2	I45877	protein-tyrosine k
1001	73.5	4.4	663	1	QRECI	colicin I receptor	1074	73	4.3	998	2	H75005	ATP-dependent prot
1002	73.5	4.4	666	2	D82511	1,4-alpha-glucan b	1075	73	4.3	1071	2	B84062	hypothetical prote
1003	73.5	4.4	721	2	T05815	hypothetical prote	1076	73	4.3	1115	2	T29012	hypothetical prote
1004	73.5	4.4	737	2	T46243	hypothetical prote	1077	73	4.3	1137	2	E86708	pyruvate carboxyla
1005	73.5	4.4	743	2	D64062	GTP diaphosphokinas	1078	73	4.3	1144	2	AB1983	probable DNA-direc
1006	73.5	4.4	780	2	A34102	von Willebrand fac	1079	73	4.3	1177	2	T16594	hypothetical prote
1007	73.5	4.4	785	2	S54016	SOK2 protein - yea	1080	73	4.3	1199	2	T23005	hypothetical prote
1008	73.5	4.4	790	2	I51638	F-cadherin - Afric	1081	73	4.3	1289	2	C70044	probable phosphoes
1009	73.5	4.4	794	2	T36972	probable membrane	1082	73	4.3	1293	2	E85557	enterobactin synth
1010	73.5	4.4	813	1	A49123	fibroblast growth	1083	73	4.3	1293	2	A90707	enterobactin synth
1011	73.5	4.4	868	2	D86349	hypothetical prote	1084	73	4.3	1311	2	T33757	hypothetical prote
1012	73.5	4.4	886	2	E75625	hypothetical prote	1085	73	4.3	1407	1	T00558	probable ABC trans
1013	73.5	4.4	891	2	T19915	hypothetical prote	1086	73	4.3	1437	2	T31093	probable protein-l
1014	73.5	4.4	899	1	GNMWM	fibronectin-bindin	1087	73	4.3	1452	1	S17669	protein-tyrosine-p
1015	73.5	4.4	1117	2	S33851	pol polyprotein -	1088	73	4.3	1484	2	T42632	breast cancer tumo
1016	73.5	4.4	1137	1	GNVSR	endopeptidase Ia h	1089	73	4.3	1615	2	B49502	multifunctional am
1017	73.5	4.4	1133	2	S12597	M polypeptide prec	1090	73	4.3	1714	1	A18644	protein-tyrosine-p
1018	73.5	4.4	1166	2	T28680	fibritrogen-bindin	1091	73	4.3	1767	2	A49502	myocerosate synth
1019	73.5	4.4	1259	2	H65233	yeFN protein - Esc	1092	73	4.3	2118	2	S72705	enoyl-l-acyl-carrie
1020	73.5	4.4	1293	1	YGECEP	enterobactin synth	1093	73	4.3	2505	1	XYRTPA	vesicular transpor
1021	73.5	4.4	1507	2	D97106	large chain of NAD	1094	73	4.3	2824	2	B53435	hypothetical prote
1022	73.5	4.4	2218	2	B84683	hypothetical prote	1095	73	4.3	3947	2	T23759	ferrichrome sidero
1023	73.5	4.4	2761	2	T21064	hypothetical prote	1096	73	4.3	3947	2	T52486	
1024	73.5	4.4	2899	2	T21546	hypothetical prote	1097	73	4.3	15281	2	S41309	
1025	73.5	4.4	2915	2	G87867	protein F36A2.13 l	1098	72.5	4.3	104	2	S36064	Ig lambda chain -
1026	73.5	4.4	3097	2	T28635	glutamate synthase	1099	72.5	4.3	110	2	S23897	T-cell receptor al
1027	73.5	4.4	107	2	B45722	anti-glycoprotein	1100	72.5	4.3	111	1	L6HULT	Ig lambda chain V-
1028	73	4.3	113	2	I46637	rearranged T-cell	1101	72.5	4.3	112	1	L1HUMA	T-cell receptor be
1029	73	4.3	113	2	B49041	T-cell receptor al	1102	72.5	4.3	114	2	I38315	T-cell receptor be
1030	73	4.3	120	2	B25429	Ig heavy chain, me	1103	72.5	4.3	114	2	I38314	T-cell receptor be
1031	73	4.3	126	2	B46538	Ig lambda chain pr	1104	72.5	4.3	115	2	S03510	T-cell receptor be
1032	73	4.3	131	1	L6HTEB	T-cell receptor ga	1105	72.5	4.3	133	2	A25777	T-cell receptor be
1033	73	4.3	135	2	S00388	hypothetical prote	1106	72.5	4.3	135	1	RKHUVY	T-cell receptor be
1034	73	4.3	162	2	E71131	peptidylprolyl iso	1107	72.5	4.3	136	2	S57877	hypothetical prote
1035	73	4.3	173	2	T27373	neu differentiatio	1108	72.5	4.3	136	2	I46635	Ig lambda chain pr
1036	73	4.3	175	2	I38408	sodium channel bet	1109	72.5	4.3	140	2	PH0132	hypothetical prote
1037	73	4.3	210	2	I49294	CD7 antigen - mous	1110	72.5	4.3	224	2	B81783	42k surface glycop
1038	73	4.3	210	2	I49294	Ig lambda chain V	1111	72.5	4.3	233	2	JH0372	Ig heavy chain VHI
1039	73	4.3	213	2	S21066	probable fibribrial	1112	72.5	4.3	249	2	S69340	hypothetical prote
1040	73	4.3	224	2	S12328	probable fibribrial	1113	72.5	4.3	250	2	D83835	hypothetical prote
1041	73	4.3	227	2	AF0869	hypothetical prote	1114	72.5	4.3	307	1	RMWSBC	T-cell receptor be
1042	73	4.3	251	2	T15495	PHP superfamily hy	1115	72.5	4.3	312	2	T33344	UDP-glucose 4-epim
1043	73	4.3	253	2	G97267	T-cell receptor al	1116	72.5	4.3	334	2	DB3768	MHC class I histoc
1044	73	4.3	267	1	RMWSC8	fibmbrial adhesin p	1117	72.5	4.3	365	2	JH0537	MHC class I histoc
1045	73	4.3	354	2	B82850	MHC class I histoc	1118	72.5	4.3	366	2	I54430	MHC class I histoc
1046	73	4.3	362	2	A45834	MHC class I histoc	1119	72.5	4.3	366	2	I61866	gene HLA-C protein
1047	73	4.3	362	2	I61907	MHC class I histoc	1120	72.5	4.3	366	2	I56034	hypothetical prote
1048	73	4.3	362	2	A45850	MHC class I histoc	1121	72.5	4.3	408	2	S76830	
1049	73	4.3	362	2	A45850	lymphocyte antigen	1122	72.5	4.3	416	1	KIVKGL	
1050	73	4.3	362	2	A45850		1123	72.5	4.3				
1051	73	4.3	362	2	I81233		1124	72.5	4.3				

1125	72.5	4.3	426	2	D42519	A20R protein - vac	1198	72	4.3	997	2	S23444	Ca2+-transporting
1126	72.5	4.3	426	2	T37408	probable 49.1K pro	1199	72	4.3	997	2	S04651	Ca2+-transporting
1127	72.5	4.3	432	2	T43476	hypothetical prote	1200	72	4.3	997	2	B31982	Ca2+-transporting
1128	72.5	4.3	460	2	T38608	hypothetical prote	1201	72	4.3	1042	1	PWRBMC	Ca2+-transporting
1129	72.5	4.3	468	1	VGBEH	glycoprotein gp13	1202	72	4.3	1042	2	A31981	Ca2+-transporting
1130	72.5	4.3	471	1	PABCA	alkaline phosphat	1203	72	4.3	1042	2	S04652	Ca2+-transporting
1131	72.5	4.3	481	2	S62427	G-protein signalin	1204	72	4.3	1042	2	A33881	Ca2+-transporting
1132	72.5	4.3	491	1	TUBOP	p-cadherin - bov	1205	72	4.3	1043	2	A31982	Ca2+-transporting
1133	72.5	4.3	502	1	A83938	lipopolysaccharide	1206	72	4.3	1135	1	GNVOH7	M polyprotein - Ha
1134	72.5	4.3	503	2	JC5287	SNP substrate-1 pr	1207	72	4.3	1135	1	GNVOH7	M polyprotein - Ha
1135	72.5	4.3	533	2	T34458	hypothetical prote	1208	72	4.3	1218	2	AD0837	ABC transport prot
1136	72.5	4.3	553	1	H46329	cell fusion glycop	1209	72	4.3	1218	2	T30293	ABC transport prot
1137	72.5	4.3	558	2	S57830	glucose-6-phosphat	1210	72	4.3	1289	2	E90098	RNA polymerase III
1138	72.5	4.3	559	2	S41806	glucose-6-phosphat	1211	72	4.3	1306	2	S25370	MSB2 protein - yea
1139	72.5	4.3	612	2	B84936	RNA polymerase sig	1212	72	4.3	1408	2	H69068	cell surface glyco
1140	72.5	4.3	619	2	A43361	Res-related trans	1213	72	4.3	1695	1	A56921	kinesin family pro
1141	72.5	4.3	641	2	G85043	hypothetical prote	1214	72	4.3	2090	2	S26058	probable transform
1142	72.5	4.3	694	2	G01161	thymopietin alpha	1215	72	4.3	2142	1	ZLVNPV	genome polyprotein
1143	72.5	4.3	723	2	T30094	hypothetical prote	1216	72	4.3	2302	2	T14328	protein-tyrosine-p
1144	72.5	4.3	760	1	S43859	Alpase - Sulfolobu	1217	72	4.3	2492	1	MNVYTD	nonstructural poly
1145	72.5	4.3	820	2	T14879	hypothetical prote	1218	72	4.3	5188	2	B85547	probable RTX fami
1146	72.5	4.3	867	2	AD1856	hypothetical prote	1219	72	4.3	5291	2	P90696	hypothetical prote
1147	72.5	4.3	899	2	B75018	hypothetical prote	1220	72	4.2	101	2	D25733	T-cell receptor al
1148	72.5	4.3	923	2	S09583	peptidylglycine mo	1221	71.5	4.2	102	2	S29588	Ig kappa chain V r
1149	72.5	4.3	976	1	TVHUKT	protein-tyrosine k	1222	71.5	4.2	113	2	S22891	T-cell receptor al
1150	72.5	4.3	980	2	A38523	genome polyprotein	1223	71.5	4.2	113	2	S03410	Ig kappa chain pre
1151	72.5	4.3	1088	1	PFRTGA	platelet-derived g	1224	71.5	4.2	139	2	RWH07A	T-cell receptor al
1152	72.5	4.3	1131	2	T15787	hypothetical prote	1225	71.5	4.2	142	2	S36310	T-cell receptor de
1153	72.5	4.3	1143	2	S46122	SNF2 protein homol	1226	71.5	4.2	148	2	A32536	T-cell receptor al
1154	72.5	4.3	1633	1	C4MS	complement C3 prec	1227	71.5	4.2	155	2	S58178	T cell antigen rec
1155	72.5	4.3	1707	2	AH2085	two-component hybr	1228	71.5	4.2	155	2	S71257	major latex protei
1156	72.5	4.3	2201	2	AH0095	probable sideropho	1229	71.5	4.2	246	2	PC4397	mucin 3 T10 - huma
1157	72.5	4.3	3283	2	AC1018	large repetitive p	1230	71.5	4.2	255	1	S48146	mucin 1 precursor,
1158	72	4.3	111	2	S26255	T-cell receptor be	1231	71.5	4.2	259	2	S60617	hypothetical prote
1159	72	4.3	111	2	S09963	Ig kappa chain V-J	1232	71.5	4.2	270	2	G84163	hypothetical prote
1160	72	4.3	136	2	S36304	T-cell receptor de	1233	71.5	4.2	291	2	J01562	hypothetical 33.9K
1161	72	4.3	138	2	PN0538	Ig heavy chain V r	1234	71.5	4.2	299	2	I46590	CD80 precursor - r
1162	72	4.3	144	2	A27577	T-cell receptor al	1235	71.5	4.2	329	2	JC5168	UDPglucose 4-epime
1163	72	4.3	171	2	S38237	hypothetical prote	1236	71.5	4.2	337	2	S65022	glucan endo-1,3-be
1164	72	4.3	259	2	P69678	involved in polyke	1237	71.5	4.2	345	2	I68749	MHC class I lympho
1165	72	4.3	281	1	S34626	translaton elonga	1238	71.5	4.2	352	2	G81921	hypothetical prote
1166	72	4.3	285	2	S36903	Fe gamma (Igc) rec	1239	71.5	4.2	354	2	G64086	glycerophosphodis
1167	72	4.3	286	2	I46021	Fe-gamma receptor	1240	71.5	4.2	365	1	S76914	translation releas
1168	72	4.3	323	1	PEPLBJ	penicillopepsin (E	1241	71.5	4.2	366	2	I37526	MHC class I histoc
1169	72	4.3	333	1	JC7713	ankyrin-repeat pro	1242	71.5	4.2	366	2	I72113	MHC histocompatib
1170	72	4.3	336	2	I49582	CD1.1 - mouse	1243	71.5	4.2	366	2	I59622	lymphocyte antigen
1171	72	4.3	350	2	I54308	MHC HLA B71 - huma	1244	71.5	4.2	366	2	I38507	MHC class I histoc
1172	72	4.3	354	2	S24437	class I histocompa	1245	71.5	4.2	370	2	A39115	glucan endo-1,3-be
1173	72	4.3	362	2	S24435	class I histocompa	1246	71.5	4.2	380	2	E87729	protein Y23H5A.4 l
1174	72	4.3	362	2	S16789	class I histocompa	1247	71.5	4.2	398	1	S45545	GTP cyclohydrolase
1175	72	4.3	365	2	I72170	MHC class I histoc	1248	71.5	4.2	398	2	H96967	protein containing
1176	72	4.3	365	2	S12406	MHC class I histoc	1249	71.5	4.2	426	2	T28563	hypothetical prote
1177	72	4.3	369	2	S12406	glucan endo-1,3-be	1250	71.5	4.2	426	2	C36850	A2IR protein - var
1178	72	4.3	386	2	A41950	retrovirus-related	1251	71.5	4.2	428	1	AJRXOD	glutamate-ammonia
1179	72	4.3	397	2	B87343	conserved hypochet	1252	71.5	4.2	436	2	A53568	methylcrotonoyl-Co
1180	72	4.3	406	2	B35878	class I major hist	1253	71.5	4.2	468	1	B84540	acid phosphatase (
1181	72	4.3	416	1	A42879	advanced glycoeyla	1254	71.5	4.2	492	2	T47720	pyruvate kinase-11
1182	72	4.3	436	2	T16638	hypothetical prote	1255	71.5	4.2	497	2	E86485	hypothetical prote
1183	72	4.3	450	1	MHDG	Ig mu chain C regi	1256	71.5	4.2	528	2	PC4025	intercellular adhe
1184	72	4.3	456	1	T38221	hypothetical prote	1257	71.5	4.2	539	2	S16989	dihydroallopsamide S
1185	72	4.3	456	1	T38221	hypothetical prote	1258	71.5	4.2	557	2	AF0274	ribulokinase (BC 2
1186	72	4.3	505	2	T07883	cellulase (BC 3.2.	1259	71.5	4.2	586	2	T19075	hypothetical prote
1187	72	4.3	520	2	A71564	hypothetical prote	1260	71.5	4.2	591	2	AB0509	oxalacetate decar
1188	72	4.3	559	2	A36187	interleukin-1 rece	1261	71.5	4.2	640	1	A50703	transferrin
1189	72	4.3	580	2	T28725	hypothetical prote	1262	71.5	4.2	640	1	A42908	transferrin A (BC 3.4.2
1190	72	4.3	592	2	T43402	probable protein k	1263	71.5	4.2	668	1	T09051	pepa protein - pse
1191	72	4.3	832	1	TJMSCP	p-cadherin precurs	1264	71.5	4.2	687	2	T09051	hypothetical prote
1192	72	4.3	838	2	T22367	hypothetical prote	1265	71.5	4.2	702	2	E69498	cyclomalodextrin
1193	72	4.3	915	2	T23937	hypothetical prote	1266	71.5	4.2	704	2	I39805	hypothetical prote
1194	72	4.3	974	1	A49714	protein-tyrosine k	1267	71.5	4.2	710	2	A96540	hypothetical prote
1195	72	4.3	994	1	A32792	Ca2+-transporting	1268	71.5	4.2	747	2	B47093	cellulase (BC 3.2.
1196	72	4.3	997	1	PWRBSC	Ca2+-transporting	1269	71.5	4.2	747	2	B47093	transforming prote
1197	72	4.3	997	2	B31981	Ca2+-transporting	1270	71.5	4.2	761	1	TVHOMB	transforming prote

1271	71.5	4.2	811	2	PN0689	connectin 1 - chic	1344	71	4.2	1330	2	B70836	hypothetical prote
1272	71.5	4.2	825	2	A59296	alpha-L-arabinofur	1345	71	4.2	1554	2	C72647	hypothetical prote
1273	71.5	4.2	828	2	S52393	beta-galactosidase	1346	71	4.2	1653	2	B91052	hypothetical prote
1274	71.5	4.2	857	2	T04208	probable anthranil	1347	71	4.2	1653	2	P85896	hypothetical prote
1275	71.5	4.2	960	1	UN0677	protein-tyrosine k	1348	71	4.2	2256	2	AD1018	large repetitive p
1276	71.5	4.2	1137	2	B90734	probable host spec	1349	71	4.2	4351	2	T00252	MEGF1 protein - ra
1277	71.5	4.2	1138	2	D85584	probable tail comp	1350	70.5	4.2	98	2	PH1061	Ig light chain v r
1278	71.5	4.2	1179	2	C36792	hypothetical prote	1351	70.5	4.2	107	2	A26945	Ig kappa chain v r
1279	71.5	4.2	1211	2	S68251	phospholipase C, i	1352	70.5	4.2	108	2	C30502	T-cell receptor de
1280	71.5	4.2	1236	2	JC7503	protein-tyrosine p	1353	70.5	4.2	115	2	B26524	Ig kappa chain v r
1281	71.5	4.2	1345	2	S55669	legumain protein 7	1354	70.5	4.2	115	2	A30995	T-cell receptor be
1282	71.5	4.2	1441	2	A86685	prophage p11 prote	1355	70.5	4.2	128	2	PN0445	Ig kappa chain pre
1283	71.5	4.2	1490	2	JC5145	DNA (cytosine-5-)-	1356	70.5	4.2	137	2	S03477	T-cell receptor al
1284	71.5	4.2	1612	2	AB1347	probable peptidogl	1357	70.5	4.2	142	2	AI0577	conserved hypotet
1285	71.5	4.2	1630	2	A53577	ascltes sialoglyco	1358	70.5	4.2	180	2	T16313	hypothetical prote
1286	71.5	4.2	1815	2	B95942	conserved hypotet	1359	70.5	4.2	225	2	AE2347	ribonuclease HII l
1287	71.5	4.2	1939	2	D97316	probable S-layer p	1360	70.5	4.2	228	2	S25575	Ig light chain - r
1288	71.5	4.2	1946	2	AC2141	serine/threonine p	1361	70.5	4.2	235	2	S25754	Ig lambda chain -
1289	71.5	4.2	3131	2	S39842	emulatin synthetas	1362	70.5	4.2	266	2	B82655	UDP-3-O-(R-3-hydro
1290	71.5	4.2	3191	2	T22945	hypothetical prote	1363	70.5	4.2	269	2	H84313	hypothetical prote
1291	71	4.2	87	2	PH1082	Ig light chain V r	1364	70.5	4.2	272	2	C75560	conserved hypotet
1292	71	4.2	98	2	S26911	Ig heavy chain V r	1365	70.5	4.2	292	2	C84461	En/spm-like transp
1293	71	4.2	115	1	KVMSL7	Ig kappa chain pre	1366	70.5	4.2	328	2	S65023	glucan endo-1,3-be
1294	71	4.2	166	2	PL0012	Ig heavy chain pre	1367	70.5	4.2	340	2	A95939	probable spermidin
1295	71	4.2	180	2	G69222	molybdenum formylm	1368	70.5	4.2	345	2	F82528	hypothetical prote
1296	71	4.2	254	2	S48547	probable membrane	1369	70.5	4.2	348	2	S09270	Ig alpha chain C r
1297	71	4.2	287	2	B69901	cell wall-binding	1370	70.5	4.2	355	2	B97795	peptide chain rele
1298	71	4.2	321	2	AC0821	probable exported	1371	70.5	4.2	372	2	T05962	cyclin A-type - Ma
1299	71	4.2	336	2	C27658	pregnancy-specific	1372	70.5	4.2	389	2	A44832	aspartate estA - Ps
1300	71	4.2	357	2	S09269	Ig alpha chain C r	1373	70.5	4.2	397	2	S52783	aspartic proteins
1301	71	4.2	362	2	JH0541	class I histocompa	1374	70.5	4.2	406	2	D90492	hypothetical prote
1302	71	4.2	362	2	JH0539	class I histocompa	1375	70.5	4.2	419	2	A36109	pregnancy-specific
1303	71	4.2	362	2	JH0540	class I histocompa	1376	70.5	4.2	424	1	A36000	sperm-binding glyc
1304	71	4.2	362	2	S56149	lymphocyte antigen	1377	70.5	4.2	445	2	A84410	hydroxymethylpyrim
1305	71	4.2	362	2	I84488	lymphocyte antigen	1378	70.5	4.2	448	2	S65260	probable membrane
1306	71	4.2	362	2	S54505	lymphocyte antigen	1379	70.5	4.2	456	2	C57742	cyclin II - maize
1307	71	4.2	362	2	I54314	MHC HLA-B39N - hum	1380	70.5	4.2	482	2	J80395	phospho-beta-galac
1308	71	4.2	362	2	S59645	HLA-B-6701 - human	1381	70.5	4.2	483	2	E71681	isocitrate dehydro
1309	71	4.2	362	2	S54298	gene HLA-B protein	1382	70.5	4.2	485	2	S36772	E-selectin - bovin
1310	71	4.2	362	2	S68850	MHC class I histoc	1383	70.5	4.2	490	2	S07375	flagellin H-1 - Sa
1311	71	4.2	364	2	D35997	MHC class I histoc	1384	70.5	4.2	520	2	A64033	hypothetical prote
1312	71	4.2	367	1	MHC	Ig mu chain C regi	1385	70.5	4.2	532	1	A28849	intercellular adhe
1313	71	4.2	368	2	D90607	hypothetical prote	1386	70.5	4.2	539	2	JH0263	carboxy-terminal p
1314	71	4.2	374	2	F69233	carbamoyl-phosphat	1387	70.5	4.2	555	2	T43847	DNA-directed RNA p
1315	71	4.2	425	2	C64523	isocitrate dehydro	1388	70.5	4.2	577	2	A95902	probable glycerol-
1316	71	4.2	427	2	T05019	hypothetical prote	1389	70.5	4.2	600	2	AH2623	60 kd inner-membra
1317	71	4.2	427	2	A11264	N-acetylmuramoyl-L	1390	70.5	4.2	600	2	G97405	60K inner-membrane
1318	71	4.2	453	2	H96798	hypothetical prote	1391	70.5	4.2	612	2	T13152	WDRI protein - hum
1319	71	4.2	459	2	T43538	zinc finger protei	1392	70.5	4.2	612	2	AF0079	DNA polymerase sig
1320	71	4.2	476	2	A70318	aldehyde dehydroge	1393	70.5	4.2	629	2	A46500	Ly-9.2 antigen - m
1321	71	4.2	481	2	JQ1147	N-acetylmuramoyl-L	1394	70.5	4.2	666	2	C90464	hypothetical prote
1322	71	4.2	509	2	AC2317	hypothetical prote	1395	70.5	4.2	682	2	T10319	envelope protein B
1323	71	4.2	511	1	VGBER4	glycoprotein C - h	1396	70.5	4.2	727	2	D75122	hypothetical prote
1324	71	4.2	513	1	A48233	polyomavirus enhan	1397	70.5	4.2	764	2	T39194	5-methyltetrahydro
1325	71	4.2	550	2	G70597	probable proteinas	1398	70.5	4.2	774	2	A39832	scabrous locus (ac
1326	71	4.2	626	2	S53871	Pmel 17 protein -	1399	70.5	4.2	782	2	AF0179	conserved hypotet
1327	71	4.2	656	2	D96831	hypothetical prote	1400	70.5	4.2	787	2	A75347	GRP pyrophosphokin
1328	71	4.2	662	2	JC7906	sucrose 1F-fructos	1401	70.5	4.2	846	1	PNECA	penicillin amidase
1329	71	4.2	681	2	S53743	glutamine-fructose	1402	70.5	4.2	856	2	S58411	protein-tyrosine k
1330	71	4.2	744	2	AF0410	GRP diaphosphokinas	1403	70.5	4.2	874	2	E97302	hypothetical prote
1331	71	4.2	771	2	T13618	hypothetical prote	1404	70.5	4.2	878	2	AD0664	hypothetical prote
1332	71	4.2	776	2	B41704	genome polypeptid	1405	70.5	4.2	879	2	S64755	N-cadherin 1 precu
1333	71	4.2	776	2	A41704	genome polypeptid	1406	70.5	4.2	905	1	IJX1C1	hypothetical prote
1334	71	4.2	796	2	A90541	hypothetical prote	1407	70.5	4.2	1043	2	F97302	M polypeptid prec
1335	71	4.2	972	1	TVRMD	macrophage colony-	1408	70.5	4.2	1133	1	A43964	M polypeptid prec
1336	71	4.2	976	1	TVMSMD	macrophage colony-	1409	70.5	4.2	1134	1	A43960	M polypeptid prec
1337	71	4.2	994	2	A48849	Ca2+-transporting	1410	70.5	4.2	1134	1	GNVU22	M polypeptid prec
1338	71	4.2	994	2	A70776	probable glns - My	1411	70.5	4.2	1210	2	S35548	DNA-directed RNA p
1339	71	4.2	1001	1	PWRBFC	Ca2+-transporting	1412	70.5	4.2	1603	1	VIRK5	vitellogenin vit-5
1340	71	4.2	1067	2	T28663	hypothetical prote	1413	70.5	4.2	1617	2	B86483	protein F55.15 (I
1341	71	4.2	1135	2	JS0605	M polypeptid - Ha	1414	70.5	4.2	1666	1	C3GP	complement C3 prec
1342	71	4.2	1142	2	GNVUPH	M polypeptid prec	1415	70.5	4.2	1804	2	A11850	serine/threonine k
1343	71	4.2	1157	2	P97255	fusion of alpha-gl	1416	70.5	4.2	2037	2	T16881	hypothetical prote

1417	70.5	4.2	3097	2	T00021
1418	70.5	4.2	3898	1	GNMVB
1419	70	4.1	110	2	B30583
1420	70	4.1	118	2	B32536
1421	70	4.1	132	2	PL0114
1422	70	4.1	132	2	S04937
1423	70	4.1	132	2	S05268
1424	70	4.1	133	2	S57886
1425	70	4.1	133	2	B30587
1426	70	4.1	135	2	JQ0472
1427	70	4.1	136	2	B45893
1428	70	4.1	224	2	C72390
1429	70	4.1	233	2	S25752
1430	70	4.1	239	2	T48937
1431	70	4.1	248	2	P00769
1432	70	4.1	261	2	S29360
1433	70	4.1	263	2	JQ0284
1434	70	4.1	275	1	HLHU10
1435	70	4.1	276	2	T47734
1436	70	4.1	294	2	H90300
1437	70	4.1	295	2	C83231
1438	70	4.1	303	1	B36227
1439	70	4.1	323	2	T50255
1440	70	4.1	327	2	JT0584
1441	70	4.1	354	2	I59308
1442	70	4.1	354	2	S24440
1443	70	4.1	361	2	I54418
1444	70	4.1	362	2	I37520
1445	70	4.1	362	2	I61860
1446	70	4.1	368	2	I55961
1447	70	4.1	373	2	T38687
1448	70	4.1	374	2	T46085
1449	70	4.1	380	1	S53307
1450	70	4.1	382	1	A70078
1451	70	4.1	385	1	G71246
1452	70	4.1	392	2	D83513
1453	70	4.1	400	1	SAVIA
1454	70	4.1	446	2	T41091
1455	70	4.1	452	2	S77538
1456	70	4.1	459	2	T37704
1457	70	4.1	485	2	AD0041
1458	70	4.1	492	2	F81823
1459	70	4.1	515	2	JC7553
1460	70	4.1	517	2	T02464
1461	70	4.1	557	2	H69678
1462	70	4.1	564	2	AH1696
1463	70	4.1	570	2	A57535
1464	70	4.1	570	2	A75201
1465	70	4.1	580	2	AE1452
1466	70	4.1	619	2	G72709
1467	70	4.1	622	2	G61197
1468	70	4.1	625	2	G70574
1469	70	4.1	632	2	T00108
1470	70	4.1	634	2	T51282
1471	70	4.1	664	2	A84716
1472	70	4.1	704	2	F87706
1473	70	4.1	729	1	A60006
1474	70	4.1	753	1	P90933
1475	70	4.1	753	2	B85782
1476	70	4.1	760	2	T24521
1477	70	4.1	804	2	S64080
1478	70	4.1	814	2	T00740
1479	70	4.1	817	2	A48721
1480	70	4.1	848	2	C70834
1481	70	4.1	883	2	S57653
1482	70	4.1	883	2	S49126
1483	70	4.1	918	2	T02759
1484	70	4.1	952	2	S64473
1485	70	4.1	955	2	S52959
1486	70	4.1	963	2	AF2119
1487	70	4.1	975	2	I48974
1488	70	4.1	978	1	A49814
1489	70	4.1	979	2	A35913

DN-cadherin - fru
 genome polypeptide
 T-cell receptor al
 T-cell receptor al
 Ig lambda chain pr
 Ig lambda chain pr
 Ig kappa chain pr
 T cell receptor al
 outer membrane pro
 T-cell receptor be
 T-cell receptor al
 hypohetical prote
 Ig lambda chain -
 hypohetical prote
 glycoprotein G - b
 Fc gamma (196) rec
 glycoprotein G - b
 MHC class I histoc
 hypohetical prote
 hypohetical prote
 conserved hypochet
 urate oxidase (EC
 hypohetical trans
 deoxyribonuclease
 class I histocompa
 class I histocompa
 MHC class I histoc
 MHC class I histoc
 MHC HLA-B18 chain
 MHC class I histoc
 hypohetical prote
 hypohetical prote
 alcohol dehydrogen
 conserved hypochet
 hypohetical prote
 hypohetical prote
 probable esterase
 large surface anti
 conserved hypochet
 serine proteinase
 zinc-finger protei
 rhamnulokinase (EC
 conserved hypochet
 inulinase (EC 3.2.
 hypohetical prote
 involved in polyke
 alpha-acetolactate
 intrileukin 1 recep
 hypohetical prote
 ABC transporter, A
 probable DNA ligase
 6-methylsalicylic
 diac-type molecula
 hypohetical prote
 beta-D-glucan exoh
 probable GTP-bind
 prolyl oligopeptid
 coat protein VP1 -
 catalase, hydrop
 hypohetical prote
 SCY1 protein - yea
 hypohetical prote
 titlin, muscle - ch
 probable endopepti
 brevicin precursor
 hypohetical prote
 hypohetical prote
 translation initia
 male-specific leth
 hypohetical prote
 receptor-protein c
 protein-tyrosine k
 regulatory factor

1490	70	4.1	988	2	T08102
1491	70	4.1	1001	2	T00532
1492	70	4.1	1016	2	T30943
1493	70	4.1	1025	2	A83186
1494	70	4.1	1089	1	S33727
1495	70	4.1	1088	1	S45917
1496	70	4.1	1133	2	B86308
1497	70	4.1	1172	2	P84572
1498	70	4.1	1189	2	T17088
1499	70	4.1	1402	2	D70634
1500	70	4.1	1409	2	T42522

ALIGNMENTS

RESULT 1
 S56749
 functional adhesion molecule precursor - human
 N/A:Accession: A59406; KWID:95326797; PIDN:AAD42050.1
 C/Spectra: Homo sapiens (man)
 C/Date: 27-Oct-1995 #sequence - revision 01-Feb-2002 #text_change 09-Jul-2004
 C/Accession: A59406; S56749
 R/Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamoto, A.;
 J. Immunol. 163, 553-557, 1999
 A/Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistributi
 A/Reference number: A59406; KWID:95326797; PIDN:AAD42050.1
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-299 <OZA>
 A/Cross-references: UNIPROT:Q9Y624; GB:AAD42050; NID:95326797; PIDN:AAD42050.1
 R/Naik, U.P.; Ehrlich, Y.H.; Kornicki, E.
 Biochem. J. 310, 155-162, 1995
 A/Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of
 A/Reference number: S56749; KWID:95374438; PMID:7646439
 A/Accession: S56749
 A/Molecule type: protein
 A/Residues: 28-49, 'X', '51-53;62-73, 'B', '75-103;123, 'F', '125-130, 'PDKXITLYLNKX', 'LT', '206, 'X'
 A/Note: the order of the peptides other than the amino terminus was not determined
 C/Genetics:
 A/Gene: JMW
 C/Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane
 F.1-25/Domain: signal sequence #status predicted <SIG>
 F.26-299/Product: junctional adhesion molecule #status predicted <MAT>

Query Match 10.6%; Score 178.5; DB 2; Length 299;
 Best local similarity 26.5%; Pred. No. 2.3e-06;
 Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY	1	MGILLGLLLGLHVTVDYGRPILEVPEVSTGPKAGVNIPTCTYDPLQGTQVLVKNLVQR	60
DB	17	LAILLCSLALGVTVAHS-SEPEVRIPEN-----NPKVLSCAV---SGFSSPVEW----	62
QY	61	GSPVITFLDSSGDHIQAKYQGRHVGHK-----VPGVBSQLSTLEMDSDSHTCSEV	115
DB	63	-----KFDGDTFLVCYNNKITASVEDRTFLPGITKSVTRR--DGTYYCMV	111
QY	116	TWQTPDGNQVVRDKITELRVQKLSVSKPTVTSSGYFTVPGQMRISLQCOAR-GSPPIIS	174
DB	112	SEEGNSYGVKVKKLVL-----VPPSKPTYNIFS-----SATTGNRAVLTSSEDDGSPSE	163
QY	175	YIVYK---QQTN-----NOPIKAVTLSTLLFKPAVIADSGSYFCTAKQVGSSEQH	222
DB	164	YTFPKDGIWPTPKSTRFASNSGYVILNPTTGLVDPDLSASDTGGRYSCEARNGYGTPT	223
QY	223	SDIVK 227	
DB	224	SNVVR 228	

RESULT 2
 I38346

elastic titin - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I38346
R:Label: S.; Kojmer, B.
Science 270, 293-296, 1995
A>Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A:Reference number: A57430; MUID:96026330; PMID:7569978
A:Accession: I38346
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 17962 <RES>
A:Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:91017426; PIDN:CAA62189.1; PID:9101
C:Genetic: GDB:TTN
A:Gene: GDB:TTN
A:Cross-references: GDB:127867; OMIM:188840
A:Map position: 2q31-2q31

Query Match 10.2%; Score 172; DB 2; Length 7962;
Best Local Similarity 27.5%; Pred. No. 0.00045;
Matches 67; Conservative 30; Mismatches 85; Indels 62; Gaps 11;

QY 16 DTGRPLLEPES-VYGPWKGVNLP-----CTYDPLQGYOVLVK-----LYRGSDP 64
DB 860 DSSGALIVQEPSPFVTPKSGKDV-LPGSAVCLKSTPQSGSTPLTRFMKGNKELVSGSCY 918
QY 65 VTFLRDSGSDHIQQAQYQGRLVSHKVPDGVSLQSLTEMDRSHYTCVWTQTPDG-- 122
DB 919 IT-----KEALSSLELVLTSTDSGTYTCV--NVAGVE 953
QY 123 ---NOVVRDKITELRVOKLSVSKPTVTTSQSGYFTVPQGRISLQCGARGSPISYIWK 179
DB 954 CSANLFFKEPAT--PFEKLEPSQ-----LLKKGDAQLACKVGTGPPIKITWFA 1000
QY 180 QQNNQEPK-----VATLSTLFRKAVINDSGSYCTACQVSGEHSNIVKVDK 234
DB 1001 NDRIRIKSSKRRMSFVESTAVLRLTVGIDSGEYMCQAEAGSDHCSSIV--IVKSP 1058
QY 235 KLLK 238
DB 1059 YFTR 1062

RESULT 3
JC7780
coxackie- and adenovirus receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
C:Accession: JC7780
R:Thoenen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res. Commun. 288, 805-808, 2001
A>Title: Characterization of a cDNA encoding the bovine coxackie and adenovirus recep
A:Reference number: JC7780
A:Contents: liver
A:Accession: JC7780
A:Molecule type: mRNA
A:Residues: 1-365 <THO>
A:Cross-references: UNIPROT:Q8MNV3; GB:A033651
C:Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Query Match 10.0%; Score 169; DB 2; Length 365;
Best Local Similarity 24.8%; Pred. No. 1.6e-05;
Matches 85; Conservative 40; Mismatches 120; Indels 98; Gaps 17;

QY 1 MGILLGLLGLHTVDPYGRPILEVPESVTPKGP-VNLPCTV-----DPLQGYQV 52
DB 1 MEHLRFLLCGVADTRGLST-TTPQMEKAKGETAIVPKFTLGPEDQGLD----- 54
QY 53 LVKMLVORGSG---DVTTLFLRDSGSDHIQQAQYQ---GRIVSHK--VPGDVSLQSLTL 103
DB 55 -LEWLSPADNKGVDQVYIY---SGDKIYDDYQDLKGRVHFTSDMSKSGDASINVTML 110
QY 104 EMDRSHYTCVWTQTPDGQNVVRDKITELRVOKLSVSKPTVTTSQSGYFTVPQ---GM 159

DB 111 QLSDITGYCKYKAPGVNKK-----KIQLTVLVPR-----SGIRCYDGSREIGN 156
QY 160 RSLSLQCAR-GSPPISYIWKQTNQBP---IXVATLSTLFRKAVINDSGSPCTAG 215
DB 157 DFKLKEPREGSLPLEYEQKLSDSQKLPTSMLEPENTSVISVKNASAYSGTYTIVN 216
QY 216 QVSGEHSNDIVFVVDSSKLLKTKTEAFTTTPPLKATSTVQSWDWTMDMDGYLGRTS 275
DB 217 RRGSDQ-----CLRLDVPPSNR-----AGTI 239
QY 276 AGRGSLPFAILLISLCCMVFTWYMYMLCRKTSQGEHYE 318
DB 240 AG-----AVIGTLALVIALIVF-----CCHKRRREKYE 270

RESULT 4
B49120
protein-tyrosine kinase (BC 2.7.1.112) dtc2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C:Accession: B49120; S18010
R:Shishido, E.; Higashijima, S.; Emori, Y.; Saigo, K.
Development 117, 751-761, 1993
A>Title: Two FGF-receptor homologues of Drosophila: one is expressed in mesodermal prim
A:Reference number: A49120; MUID:93321617; PMID:8330538
A:Accession: B49120
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-1052 <SHI>
A:Cross-references: UNIPROT:Q09147; GB:X74031; GB:S63797; NID:9397600; PIDN:CAA52190.1;
A:Experimental source: pupa
A>Note: sequence extracted from NCBI backbone (NCBIN:135151, NCBI:135153)
R:Shishido, E.; Emori, Y.; Saigo, K.
FEBS Lett. 289, 235-238, 1991
A>Title: Identification of seven novel protein-tyrosine kinase genes of Drosophila by th
A:Reference number: S17552; MUID:92008631; PMID:1915852
A:Accession: S18010
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 869-922 <SH2>
C:Genetic: GDB:1052
A:Gene: FlyBase:bc1; dtc2
A:Cross-references: FlyBase:FBgn0005592
C:Superfamily: protein kinase homology
C:Keywords: ATP; growth factor receptor; phosphotransferase; tyrosine-specific protein k
F:118-726/Region: protein kinase ATP-binding motif

Query Match 8.5%; Score 143.5; DB 2; Length 1052;
Best Local Similarity 23.4%; Pred. No. 0.0055;
Matches 71; Conservative 44; Mismatches 119; Indels 69; Gaps 14;

QY 16 DTGRPILE-----VPESVTPGPKGVNLPCT-YDP-LQGYTQVLVVKLVORGSDP 64
DB 130 DLFPPLNRSRLKLLQPLPKTVQRTAGLFGQNCSPMDPKG--VNISWL----- 179
QY 65 VTFLRDSGSDHIQQAQYQGRLVSHKVPDGVSLQSLTEMDRSHYTCVWTQTPDGQ 124
DB 180 -----HIDPQILGGRIRIK--RSLVLVGLQLPDADASYCELCYE-----OD 221
QY 125 VVRDKITELRVOKLSVSKPTVTTSQSGYFTVPQGRISLQCGARGSP--PPISYIWKQ 181
DB 222 QQRNPTQLEVISRKHVTPMLKGVPRNTSIALGDNVSIIECLLSDSALEPKITWL-HKGN 280
QY 182 TNN-----QEPKATVLTSLFKPAPV-----ADSSYPTAGQVSGE 222
DB 281 ADNIDDLQRLREOSQLPVDVTRLITRMDPQVILGAVLMBDGGWYICIAENQGRIVA 340
QY 223 SDIVFVVDSSKLLKTKTEAFTTTPPLKATSTVQSWDWTMDMDGYLGRTSAGRSKL 282
DB 341 ASYVDLSPSPSDITTYVITTT--TTTVASPIPTASTGEDND--DVENPAADSGGVGP-- 393

OY 283 PVF 285
Db 394 PVF 396

RESULT 5

SI8252
heparan sulfate proteoglycan - mouse
N/Alternate names: perlecan
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 12-Jul-2004
R/Accession: SI8252; A:1917; B3191; S66460
R/Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; He
J. Biol. Chem. 266, 22939-22947, 1991
A/Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteogly
adhesion molecule.
A/Reference number: SI8252; MUID:92078153; PMID:1744087
A/Accession: SI8252
A/Molecule type: mRNA
A/Residues: 1-3707 <NOC>
A/Cross-references: UNIPROT:Q05793; EMBL:M717174; NID:g200295; PIDN:AAA39911.1; PID:g2002
R/Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hase
J. Biol. Chem. 263, 16379-16387, 1988
A/Title: Identification of cDNA clones encoding different domains of the basement membra
A/Reference number: A92680; MUID:89034110; PMID:2972708
A/Accession: A31917
A/Molecule type: mRNA
A/Residues: 940-1601 <NOC2>
A/Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253
A/Accession: B31917
A/Molecule type: mRNA
A/Residues: 1870-2600 <NOC3>
A/Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301
R/Schulze, B.; Mann, K.; Bactletter, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A/Title: Structural properties of recombinant domain III-3 of perlecan containing a glob
A/Reference number: S66460; MUID:95377282; PMID:7649154
A/Accession: S66460
A/Molecule type: protein
A/Residues: 1272-1274, 'X', 1276, 'X', 1278-1279 <SCH>
C/Keywords: glycoprotein
F/159-334/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F/285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F/325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F/368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F/764-811/Domain: laminin-type EGF-like homology <LEG>
F/1159-1206/Domain: laminin-type EGF-like homology <LEG7>
F/1563-1610/Domain: laminin-type EGF-like homology <LEG8>
F/1613-1668/Domain: laminin-type EGF-like homology <LEG8>
F/3163-3198/Domain: EGF homology <EGF>
F/3370-3423/Domain: laminin G repeat homology <EGF7>
F/3464-3492/Domain: EGF homology <EGF7>
F/1556, 1891, 2336, 2394, 2427/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.3%; Score 139.5; DB 2; Length 3707;
Best Local Similarity 25.1%; Pred. No. 0.055;
Matches 66; Conservative 31; Mismatches 105; Indels 61; Gaps 14;
OY 13 LTVDVT---YGRPLFVPSVTGPMKGDVNLPTCYDPLQGYTVLVKMLVQRSGDPVTFIF 68
Db 2521 LIYDTGVAPCTPQVQVES-----ELTLEA-----GHTATL--HCAATGPPPT-- 2553
OY 69 LRDSGGHIOQAKYQGRHLVSHKVPQDVSLQSLTEMDRSHYTCVETWTQTPDGNQVVRD 128
Db 2564 -----IHWSKRRAPLPMQHRIEGN-TLIVPRVAQDSQGYICNAT-----NSAGHT 2608
OY 129 KITELRVQKLSVSKPYTTSQSGVFTVQ-----GKRISQCARSPISYIWTYQQT 182
Db 2609 EATV---LHVESPP-----YATIPERTSAQPNLVQCLAHGTPPLYQM--SLV 2656
OY 183 NNQPIKAVATLSTLL-FKPAVIADSGSYCTAKGVSGEQRSDIVKFPVVKSSKLTKTKT 241
Db 2657 GGVLPEKAVVRNQILRLRLEPTVPEDSGRYRCQVSRVGSAA--AFAYQLVQSSSNLPTDS 2714

OY 242 ----EARTTWTYPLKATSTYKOS 260
Db 2715 IPGASTPTVQVTPQLERTRIGAS 2737

RESULT 6

PN0568
connectin 3B - chicken (fragment)
N/Alternate names: CN3B protein
C/Species: Gallus gallus (chicken)
C/Date: 03-May-1994 #sequence revision 07-Oct-1994 #text_change 09-Jul-2004
R/Accession: PN0568
R/Maruyama, K.; Endo, T.; Kume, H.; Kawamura, Y.; Kanazawa, N.; Nakauchi, Y.; Kimura, S.
Biochem. Biophys. Res. Commun. 194, 1288-1291, 1993
A/Title: A novel domain sequence of connectin localized at the 1 band of skeletal muscul
A/Reference number: PN0568; MUID:93356802; PMID:8352787
A/Accession: PN0568
A/Molecule type: mRNA
A/Residues: 1-1323 <NAB>
A/Cross-references: UNIPROT:Q08476; DDBJ:D16541; NID:g391629; PID:dl004495; PID:g391630
A/Experimental source: skeletal muscle
C/Comment: This protein string-like single molecule spans from the 2 line to the M line

Query Match 8.2%; Score 138.5; DB 2; Length 1323;
Best Local Similarity 21.4%; Pred. No. 0.018;
Matches 61; Conservative 38; Mismatches 117; Indels 69; Gaps 10;

OY 22 ILFVPSV---TGPMKGDVNLPTCYDPLQGYTVLVKMLVQRSGDPVTFIFLRDSSGDHIQ 78
Db 143 ILRLPNSKLEDOQOYSHINDSGDNCHAIITLEPPYVTFLEPQVTVGVSASLQCC 202
OY 79 QAK-----YQ-----RLVSHKVPQDVSLQSLTEMDRSHYTCVETWTQTP 120
Db 203 VAGTPEMIVSWYKDTFLRGTATVKNHFKNQV--ATLVFSQVSDSGEYICKVENTVG 259
OY 121 DGNQ-----VVRKITELRVQKLSVSKPYTTSQSGVFTVQPMRISLQCARSPISY 175
Db 260 EATSSSLITVQERLRLPSPFTRKLRDVEIV-----GLPVTFGIAGSEPIEV 307
OY 176 IWTQQTNNQPIKAVAT--LSTLLFKPAVIADSGSYCTAKGVSGEQRSDIVKFPV 230
Db 308 SWRKDNVRVEDNVHTSFIDNVAILQILRTDLSLNGQYCTSMAGT-----A 357
OY 231 KDSSKLTKTEAPTTWTYPLKATSTYKOSDWTTMDGYLGTS 275
Db 358 SSSGKLVLTGKTPPFDPPTI-----TPVDGIIGESA 389

RESULT 7

T42633
connectin/citin - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 09-Jul-2004
R/Accession: T42633
R/Iejima, H.; Ohnaka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.; M
Biochem. Biophys. Res. Commun. 223, 160-164, 1996
A/Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/citin r
A/Reference number: Z22221; MUID:96254045; PMID:8660363
A/Accession: T42633
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-4162 <YAJ>
A/Cross-references: UNIPROT:Q08918; EMBL:D83390; NID:g1513029; PIDN:BA11908.1; PID:g15
A/Experimental source: breast muscle
C/Keywords: skeletal muscle

Query Match 8.2%; Score 138.5; DB 2; Length 4162;
Best Local Similarity 21.4%; Pred. No. 0.076;
Matches 61; Conservative 38; Mismatches 117; Indels 69; Gaps 10;
OY 22 ILFVPSV---TGPMKGDVNLPTCYDPLQGYTVLVKMLVQRSGDPVTFIFLRDSSGDHIQ 78

Db 3895 ILB1PNSKLEDOQGYSCHEIENDSGDNCHGATITLLEPPYFVTPLEPVQVTDGDSASIQQC 3954
QY 79 QAK-----YQG-----RLVSHKVPGDVSLQSTLEMDRSHYTCETVMTQTR 120
Db 3955 VAGTPEMVSWYGDTRGTATVKNHFKQV---ATLVSYQVSDSGEITCKVENTWG 4011
QY 121 DGNQ-----VVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMKRLSLQCGARSPISY 175
Db 4012 EATSSSLTLVQGERKLPPSPFRKLRDHYETV-----GLPVPFGDGIAGSERIEV 4059
QY 176 IWKQQTNNQEPKIVAT--LSTLFRKAVIADG--GSYFCTAKGVGSEHSDIYKVV 230
Db 4060 SWEKDMVRVKEEDVNVHSPFDNVAIIQILKTDLSLWQYTCFASNAIGT-----A 4109
QY 231 KDSKLLKTKTEAPTMTVTPVKATSTYKQSDWTDMDGVLGERTS 275
Db 4110 SSSGKLVLRGKTPPPFDTPF-----TPVDGITGESA 4141

RESULT 8

T08678

hypothetical protein DKFZp56411922.1 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: T08678

R/Vambutt, R.; Heubner, D.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A/Reference number: Z16469

A/Accession: T08678

A/Molecule type: mRNA

A/Residues: 1-584 <MAN>

A/Cross-references: UNIPROT:Q9Y3Y8; EMBL:AL049946

A/Experimental source: fetal brain; clone DKFZp56411922

C/Genetics:

A/Note: DKFZp56411922.1

Query Match 8.1%; Score 136; DB 2; Length 584;

Best Local Similarity 22.4%; Pred. No. 0.0099;

Matches 53; Conservative 37; Mismatches 99; Indels 48; Gaps 8;

QY 35 GDNVNLCTYDPLQGYOVLVKLVQKSDPTVFLADSGSDHIIQQAQYQGRHSHKVP 94
Db 15 GDLKVCV--ATGLPPEISWSLPGSLVNSMOSDSGGRYR-----YVFN 61
QY 95 DVSILSTLEMDRSHYTCETVMTQTRPDGNQVDRKITELVQKLSVSKP--TVTTGSGYGR 153
Db 62 NGTLVNEVGMKEGDTCPAE-----NOVGKD--EMKVRKVVTAPTTNKTCIAV 112
QY 154 TVPQGRISLQCGARSPISYIYV---KQOTNQEPIKAVTSLTFKPAVIADSGSY 209
Db 113 QVYGVVVTVACBAKGPMPKVTWLSPTNKVIRPTSEKQYIQDGTLLIQAKRSDSGNV 172
QY 210 FCTAKQVGEQH-----SDIVKPVVQSSKLLKTKTA--PT 245
Db 173 TCLVRNSAGSDRTWIHVNVQPKINGNPITTVREIAAGSRKLDICKAGIPT 229

RESULT 9

T20992

hypothetical protein F15G9.4a - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T20992; T24733

R/Sulston, J.

submitted to the EMBL Data Library, December 1994

A/Reference number: Z19355

A/Accession: T20992

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-5175 <MTL>

A/Cross-references: UNIPROT:Q810L3; EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F1

R/Kerhaw, J.

submitted to the EMBL Data Library, December 1994

A/Reference number: Z19929

A/Accession: T24733

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-5175 <MT2>

A/Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a

A/Experimental source: clone T0989

C/Genetics:

A/Gene: F15G9.4a

A/Map position: X

A/Intons: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/

Query Match 7.9%; Score 133.5; DB 2; Length 5175;

Best Local Similarity 22.9%; Pred. No. 0.24;

Matches 48; Conservative 36; Mismatches 93; Indels 33; Gaps 6;

QY 76 HIQAKYQGRHSHKVPDVSILQSTLEMDRSHYTCETVMTQTRPDGNQVDRKITELV 135
Db 2796 HAHDESVOQVITTSKTAANEKTLVNTIQLDDEGFTYC-----TAVNEGITKKFPKLV 2850
QY 136 -----QKLSVSKPTVTGSGYGFVPOGMKRLSLQCGARSPISYIYWKQQTNNQ 186
Db 2851 IETPVFLDQKL-----YPIILGRILTDCSATGTPTTILFMKDGRLNE 2896
QY 187 PIKVAFL--STLFRKAVIADSGSYFCTAKGVGSEHSDIYKVV--KQSSKLLKTKTA 243
Db 2897 SDEVLDIGSTLVINDPQKEBERGYTCIAENKGRSEKDMVAVLLPPLKSKEMINVEQA 2956
QY 244 --PTMTVTPVKATSTYKQSDWTDMDGYL 271
Db 2957 GBLTLKCPIDTSGVHTWSRQFGDGL 2986

RESULT 10

T43290

hemiscentin precursor - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C/Accession: T43290; T20993; T24734

R/Vogel, B.E.; Hedgecock, E.M.

submitted to the EMBL Data Library, June 1998

A/Description: Hemiscentin is required for hemidesmosome mediated cell adhesion and germ-

A/Reference number: Z22396

A/Accession: T43290

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-5198 <VOG>

A/Cross-references: UNIPROT:O76518; EMBL:AF074901; PIDN:AAC26792.1

R/Sulston, J.

submitted to the EMBL Data Library, December 1994

A/Reference number: Z19355

A/Accession: T20993

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-5198 <MTL>

A/Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b

A/Experimental source: clone F15G9

R/Kerhaw, J.

submitted to the EMBL Data Library, December 1994

A/Reference number: Z19929

A/Accession: T24734

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-5198 <MT2>

A/Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b

A/Experimental source: clone T0989

C/Genetics:

A/Gene: him-4; F15G9.4b

A/Map position: X

A/Intons: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;

A:Gene: GDB:PCGF3B
A:Map position: 5g31-5g32
A:Cross-references: GDB:120710; OMIM:173410
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology
C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodimer
F:1-32/Domain: signal sequence #status predicted <Sig>
F:33-1106/Product: platelet-derived growth factor receptor beta #status predicted <MNT>
F:33-531/Domain: extracellular #status predicted <EXT>
F:47-102/Domain: immunoglobulin homology <IMM1>
F:142-192/Domain: immunoglobulin homology <IMM2>
F:228-293/Domain: immunoglobulin homology <IMM3>
F:429-510/Domain: immunoglobulin homology <IMM4>
F:535-555/Domain: transmembrane #status predicted <TM>
F:556-1106/Domain: intracellular #status predicted <INT>
F:598-965/Domain: protein kinase homology <KIN>
F:606-614/Region: protein kinase ATP-binding motif
F:45: 89, 103, 215, 230, 292, 307, 354, 371, 468, 479/Binding site: carbohydrate (Asn) (covalent)
F:54-100, 149-190, 235-291, 436-508/Disulfide bonds: #status predicted
F:634/Active site: lys #status predicted
F:857/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 7.9%; Score 133; DB 1; Length 1106;
Best Local Similarity 21.4%; Pred. No. 0.038;
Matches 60; Conservative 41; Mismatches 92; Indels 88; Gaps 11;

OY 23 LEVVESTGPM-----KGVNLPCTYPPLOGYOVLYKMLVQRSDPVTITLRDSSG 74
DB 145 ITICRYTDPDLVLTLEHKGDVALPVPYHQRFSGI----- 182
OY 75 DHIOQAQOGELSHKVPDGVSLQSTLEMDRSHYTCETVQTDPGQGVNRDKITELR 134
DB 183 -----FEDSYICKTTIGD-----REVDSDAVI-----VRLQ 210
OY 135 VQKLVSERPTVTGSGYGFYVPGMRISLQCOARGSPISYIV-YKQOTNNQ--EPIKVA 191
DB 211 VSSINVSVMNQ-----VROGENITLMCIYIGNVVMFEMWYPRKESGRLEVPYTFD 264
OY 192 TL-----STLFKPVAVIDSGSYFCTAKQNGSEBQSDIVKFKVQSSKLTKEAP 244
DB 265 LIDPMYHIRSTLHPSALEBDSGYTCNVATESVNDHDEKAINITVVESSG-VYRLGLEVG 323
OY 245 TTMTPPLKATSTVQKSWD-----WTTMDGILGETSAG 277
DB 324 TLQPAELHRSRTLQVFEAVPPTVTLWPKD-NRTLGDSSSAG 363

RESULT 12
C42632
cell adhesion molecule apCAM (clone d12) - California sea hare
C:Species: Aplysia californica (California sea hare)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: C42632
R:Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 236, 648-644, 1992
A:Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plasticity
A:Reference number: A42632; MUID:92263095; PMID:1565176
A:Accession: C42632
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-765 <MAV>
A:Cross-references: UNIPROT:Q9TMA4
A:Experimental source: CNS
A:Note: sequence extracted from NCBI backbone (NCBIP:101351)
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm

Query Match 7.8%; Score 132.5; DB 2; Length 765;
Best Local Similarity 20.7%; Pred. No. 0.026;
Matches 54; Conservative 31; Mismatches 63; Indels 113; Gaps 10;

OY 104 EMDRSHYTCV-----TWQTPGQGVNRDKITELKVLKSVSKPT-----VTTGSG 150
DB 230 KVGDEVKITTCATGVPPTTQFKKGDVMTDEMANNVGLTIINPLKTTDOATYTCIAITNGK 289

QY 151 YGFT-----VP-----OGMRISLOCARSPPISTYI----- 177
|||
|||
Db 290 -GFAESSNTLDVAVPPTIEDMEETDAVSGOELITCTAGADPEPSYIMKDDPGQASSTD 348
QY 178 -----YKQNTNOEPKIVATLST-LLFKPAVIADSGSYFCTAKQGVSEQSDIYK 228
|||
|||
Db 349 GIVNKGPTYEKVSNDMEKTVAQHMTFKPVTYQDAGTYICTAFSLVGSANKT--VKL 406
QY 229 VVK-----DSSKLAKTKT 241
|||
|||
Db 407 TVQYKPNFPTDFKEREFFGMRGHKANLTCQANANPVATIEWMPDAENPDDYSKAVRIYN 466
QY 242 EAPTTMTYPLKATSTYKQSWD 262
|||
|||
Db 467 EAPYTI-----NMLQKWD 479

RESULT 13

B42632
cell adhesion molecule apCAM (clone d19) - California sea hare
C/Species: Aplysia californica (California sea hare)
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: B42632
R/Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 256, 638-644, 1992
A/Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plastic
A/Reference number: A42632; PMID:92263095; PMID:1585176
A/Accession: B42632
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-812 <MAY>
A/Cross-references: UNIPROT:Q9TWA5
A/Note: sequence extracted from NCBI backbone (NCBIP:101346)
C/Superfamily: neutral cell adhesion molecule; fibronectin type III repeat homology; immu

Query Match 7.8%; Score 132.5; DB 2; Length 812;
Best Local Similarity 20.7%; Pred. No. 0.028;
Matches 54; Conservative 31; Mismatches 63; Indels 113; Gaps 10;

QY 104 EMDRSHYTCV-----TWQTPDGNQVVRDKITELRVQKLSVSKPT-----VTTGSG 150
|||
|||
Db 230 KVGDEVKITCQATGVPPPTQFKKGDVMTDEMVGVLINPLKTTDQATYTCIATNKG 289
QY 151 YGFT-----VP-----OGMRISLOCARSPPISTYI----- 177
|||
|||
Db 290 -GFAESSNTLDVAVPPTIEDMEETDAVSGOELITCTAGADPEPSYIMKDDPGQASSTD 348
QY 178 -----YKQNTNOEPKIVATLST-LLFKPAVIADSGSYFCTAKQGVSEQSDIYK 228
|||
|||
Db 349 GIVNKGPTYEKVSNDMEKTVAQHMTFKPVTYQDAGTYICTAFSLVGSANKT--VKL 406
QY 229 VVK-----DSSKLAKTKT 241
|||
|||
Db 407 TVQYKPNFPTDFKEREFFGMRGHKANLTCQANANPVATIEWMPDAENPDDYSKAVRIYN 466
QY 242 EAPTTMTYPLKATSTYKQSWD 262
|||
|||
Db 467 EAPYTI-----NMLQKWD 479

RESULT 14

A42632
cell adhesion molecule apCAM (clone d19) - California sea hare
C/Species: Aplysia californica (California sea hare)
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A42632
R/Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 256, 638-644, 1992
A/Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plastic
A/Reference number: A42632; PMID:92263095; PMID:1585176
A/Accession: A42632
A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-932 <MAY>
A/Cross-references: UNIPROT:Q9TWA6

A/Experimental source: CNS
A/Note: sequence extracted from NCBI backbone (NCBIP:101342)
C/Superfamily: neutral cell adhesion molecule; fibronectin type III repeat homology; immu

Query Match 7.8%; Score 132.5; DB 2; Length 932;
Best Local Similarity 20.7%; Pred. No. 0.033;
Matches 54; Conservative 31; Mismatches 63; Indels 113; Gaps 10;

QY 104 EMDRSHYTCV-----TWQTPDGNQVVRDKITELRVQKLSVSKPT-----VTTGSG 150
|||
|||
Db 230 KVGDEVKITCQATGVPPPTQFKKGDVMTDEMVGVLINPLKTTDQATYTCIATNKG 289
QY 151 YGFT-----VP-----OGMRISLOCARSPPISTYI----- 177
|||
|||
Db 290 -GFAESSNTLDVAVPPTIEDMEETDAVSGOELITCTAGADPEPSYIMKDDPGQASSTD 348
QY 178 -----YKQNTNOEPKIVATLST-LLFKPAVIADSGSYFCTAKQGVSEQSDIYK 228
|||
|||
Db 349 GIVNKGPTYEKVSNDMEKTVAQHMTFKPVTYQDAGTYICTAFSLVGSANKT--VKL 406
QY 229 VVK-----DSSKLAKTKT 241
|||
|||
Db 407 TVQYKPNFPTDFKEREFFGMRGHKANLTCQANANPVATIEWMPDAENPDDYSKAVRIYN 466
QY 242 EAPTTMTYPLKATSTYKQSWD 262
|||
|||
Db 467 EAPYTI-----NMLQKWD 479

RESULT 15

S26180
neurofascin - chicken
C/Species: Gallus gallus (chicken)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S26180
R/Volkmer, H.; Hasel, B.; Wolff, J.M.; Frank, R.; Rathjen, F.G.
J. Cell Biol. 118, 149-161, 1992
A/Title: Structure of the axonal surface recognition molecule neurofascin and its relat
A/Reference number: S26180; PMID:92317154; PMID:1377696
A/Accession: S26180
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1272 <VOL>
A/Cross-references: UNIPROT:Q42414; EMBL:X65224; NID:G63659; PTDN:CAA46330.1; PTD:G6366C
C/Superfamily: neutral cell adhesion molecule I1; fibronectin type III repeat homology; 1

Query Match 7.8%; Score 132.5; DB 2; Length 1272;
Best Local Similarity 22.2%; Pred. No. 0.049;
Matches 51; Conservative 38; Mismatches 88; Indels 53; Gaps 7;

QY 22 ILEVESYVPGKGVNLPCTYDPLQGYQVVKMLVGRGSDPVITFLRDSGDHIQAK 81
|||
|||
Db 150 VIEVDEG-----APLSIQCNPP-----GLPPVIFWSSMBPIHDX 188
QY 82 -----YQGRILVSHKVPDGVSLQS-----TLEMDRSHYTCVETWQTPDGNQVVRDK 129
|||
|||
Db 189 RVSGQNGDLYPSNWLQDAQTDYSCNARFHFHTHTIQKRPYTLKTKKPPHNETSLRNH 248
QY 130 ITELNVQKLSVSKPT--VTTGSGYPTVPOGMRISLOCARSPPISTYIMYK----- 179
|||
|||
Db 249 TMTSARGVETPTSPMRYGTSSQOMVLRGVDLLCTASVPAVDIMWYKKGELPAG 308
QY 180 --QNTNOEPKIVATLSTLLFKPAVIADSGSYFCTAKQGVSEQSDIYK 227
|||
|||
Db 309 KTKLENPKALAINSVS-----EDSGEFCLASNMGSIRHTISVR 350

Search completed: January 4, 2005, 06:07:47
Job time : 57 secs

Tue Jan 4 06:38:27 2005

us-10-767-374-2.rpx

Page 17

17

17

THIS PAGE BLANK (USPTO)